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106111

From: Salimi, Ali
Sent: Thursday, October 16, 2003 3:46 PM
To: STIC-Biotech/ChemLib
Subject: 08/913,644

Can you please conduct a search including interference search for the application serial no. 08/913,644, for the following:

SEQ ID NO: 2, and 4

Thanks!

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Edward Hart
Technical Info. Specialist
STIC/Biotech
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Searcher: _____
Phone: _____
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Date Picked Up: 10/13/03
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Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
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Sequence Sys.: _____
WWW/Internet: _____
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STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact*:

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 - Circ. Desk



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OM protein - protein search, using sw model

Run on: October 17, 2003, 10:47:19 ; Search time 62.8512 Seconds
(without alignments)
1280.394 Million cell updates/sec

Title: US-08-913-644-2

Perfect score: 2733
Sequence: 1 MALMRPSDMVTYTLPPPSVAR.....APSATTSSRPAAKRVRRARK 507

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database :
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3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2733	100.0	507	17 AAW05843	Human papillomavir
2	2705	99.0	568	21 AAB23927	Human papillomavir
3	2705	99.0	568	22 AAB98429	Human papillomavir
4	2694	98.6	500	23 AAO18098	HPV type 18 L1 pro
5	2457.5	89.9	536	22 AAB98442	Human papillomavir
6	1851	67.7	534	22 AAB98454	Human papillomavir
7	1834.5	67.1	504	22 AAB98436	Human papillomavir
8	1831	67.0	505	24 AAB75800	Human papillomavir
9	1826	66.8	505	20 AAT08019	Human papilloma vi

10	1826	66.8	505	21 AAT57720	Human papillomavir
11	1826	66.8	505	23 AAB77478	HPV16-L1 1. Human
12	1826	66.8	505	23 AAB77479	HPV16-L1 2. Human
13	1826	66.8	531	22 AAB98422	Human papillomavir
14	1825	66.8	505	24 AAB75799	Human papillomavir
15	1824	66.7	505	14 AAB38807	HPV1 L1. Bovine p
16	1824	66.7	505	19 AAB54034	HPV16 L1 gene prot
17	1824	66.7	505	19 AAB53487	Human papillomavir
18	1824	66.7	505	19 AAB53903	HPV16 L1 capsid pr
19	1824	66.7	505	19 AAB44143	Human papillomavir
20	1824	66.7	505	20 AAB96747	Human papillomavir
21	1824	66.7	505	21 AAB53579	HPV16 L1 protein -
22	1818	66.5	505	19 AAB63116	Human papillomavir
23	1808	66.2	505	14 AAB38808	HPV1 L1. Human pa
24	1808	66.2	505	14 AAB54073	HPV16 L1 gene prot
25	1808	66.2	505	19 AAB53486	Human papillomavir
26	1808	66.2	505	19 AAB44142	Human papillomavir
27	1808	66.2	505	20 AAB96748	Human papillomavir
28	1808	66.2	505	21 AAB53580	HPV16 L1 protein.
29	1801	65.9	531	21 AAB23925	Human papillomavir
30	1791	65.5	499	22 AAB98449	Human papillomavir
31	1789.5	65.5	497	21 AAB71464	Chimeric biotin-bi
32	1789.5	65.5	499	21 AAT71465	Chimeric biotin-bi
33	1786	65.3	532	23 AAB77483	HPV16-L1/E7 fusion
34	1785.5	65.3	533	23 AAB77482	HPV16-L1/E7 fusion
35	1783	65.2	533	23 AAB77481	HPV16-L1/E7 fusion
36	1778	65.1	501	21 AAB99981	HPV 6 L1 protein m
37	1774	64.9	501	18 AAT15111	Human HPV6 L1 prot
38	1770	64.7	501	18 AAB32080	Human HPV6 L1 prot
39	1769	64.7	501	18 AAT15110	Human HPV6 L1 prot
40	1768.5	64.7	500	18 AAT18631	Human HPV6 L1 prot
41	1768.5	64.7	500	21 AAB99976	Human papillomavir
42	1768.5	64.7	500	21 AAB99979	HPV 6 L1 protein m
43	1768.5	64.7	500	22 AAB98397	Human papillomavir
44	1768.5	64.7	500	22 AAB98406	Human papillomavir
45	1768.5	64.7	500	24 AAO16089	Human papillomavir

ALIGNMENTS

RESULT 1
ID AAW05843 standard; Protein; 507 AA.
AC AAW05843:
XX
XX 28-JAN-1997 (first entry)
XX
DE Human papillomavirus type 18 L1 capsid protein.
XX
XX HPV-18: L1 gene; capsid protein; vaccine; diagnosis; vector;
KW antibody; serotyping; cervix carcinoma.
XX
XX Human papillomavirus type 18.
OS
OS WO629413-A2.
PN
XX 26-SEP-1996.
PD
XX
XX 18-MAR-1996; 96WO-0503649.
PE
XX
XX 22-MAR-1995; 95US-0409122.
PR 22-MAR-1995; 95US-0408669.
XX
XX (MERT) MERCK & CO INC.
PA
XX George HA, Hofmann KU, Jansen KU, Joyce JG, Neepier MP;
PI WPI: 1996-443188/44.
XX N-PSDB; AAT40119.
DR
XX DNA encoding human papilloma virus 18, esp. L1 and L2 capsid

proteins - and related vectors and antibodies, useful in protective vaccines, for serotyping HPV infections and as therapeutic agents

Claim 2; Fig 1; 46pp; English.

The L1 major capsid protein (AA05843) of human papillomavirus type 18 (HPV18) has a mol.wt. of 55-60 kDa and is thought to incorporate most of the L2 minor capsid protein (AA05844). Its amino acid sequence was deduced from a genomic clone (AAT40119) isolated from human cervical carcinoma SW756 cells. Recombinant L1 and L2 proteins can be produced in transformed host cells and used in vaccines for protection against HPV18; this HPV type is associated with invasive carcinomas of the cervix, vagina, vulva and anal canal. Virus-like particles composed of recombinant L1 or L1+L2 can be produced in yeast for use as vaccines.

Sequence 507 AA;

Query Match 100.0%; Score 2733; DB 17; Length 507;
Best Local Similarity 100.0%; Pred. No. 7e-250;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MALMRPSDNTVYLPPPSVAVRVNTDDYVTRTSIFYHAGSSRLTVGNPFYFVPAAGGNKQ 60
DB 1 MALMRPSDNTVYLPPPSVAVRVNTDDYVTRTSIFYHAGSSRLTVGNPFYFVPAAGGNKQ 60
QY 61 DIPVSAVQYVRFVQVLPDPKFKGLPDSIYNPETQRLWMACAGVEIGROPGLGVLSGH 120
DB 61 DIPVSAVQYVRFVQVLPDPKFKGLPDSIYNPETQRLWMACAGVEIGROPGLGVLSGH 120
QY 121 PFYKKLDDTSSHAATSVSEVDVNDVSVYKQIOLCTLGCAPAIGEHMAKGTACKSRPL 180
DB 121 PFYKKLDDTSSHAATSVSEVDVNDVSVYKQIOLCTLGCAPAIGEHMAKGTACKSRPL 180
QY 121 PFYKKLDDTSSHAATSVSEVDVNDVSVYKQIOLCTLGCAPAIGEHMAKGTACKSRPL 180
DB 121 PFYKKLDDTSSHAATSVSEVDVNDVSVYKQIOLCTLGCAPAIGEHMAKGTACKSRPL 180
QY 181 SQGDCPPLLEKNTVLEGDVNDVYTGAMDFSTLQDKCEVPLDQCISCKYPDYLOMSAD 240
DB 181 SQGDCPPLLEKNTVLEGDVNDVYTGAMDFSTLQDKCEVPLDQCISCKYPDYLOMSAD 240
QY 181 SQGDCPPLLEKNTVLEGDVNDVYTGAMDFSTLQDKCEVPLDQCISCKYPDYLOMSAD 240
DB 181 SQGDCPPLLEKNTVLEGDVNDVYTGAMDFSTLQDKCEVPLDQCISCKYPDYLOMSAD 240
QY 241 PYGDSMFFCLAREDLFAHFNRAGTMDYTPQSLYIKGTGMRASPGSCYVSPSPSGSIV 300
DB 241 PYGDSMFFCLAREDLFAHFNRAGTMDYTPQSLYIKGTGMRASPGSCYVSPSPSGSIV 300
QY 301 TSQSOLFNRKPYWLKKAOGHNNGICMHNOLFVTVVDTTRSTNLITCASQSPVPGQYDATK 360
DB 301 TSQSOLFNRKPYWLKKAOGHNNGICMHNOLFVTVVDTTRSTNLITCASQSPVPGQYDATK 360
QY 361 FKQYSRHVEEYDLOFIQOLCTITLTADVMSYIHSNSSLIEDMNGVPPPTTSLVDTYR 420
DB 361 FKQYSRHVEEYDLOFIQOLCTITLTADVMSYIHSNSSLIEDMNGVPPPTTSLVDTYR 420
QY 421 FVQSVAILTCQKDAAPAEKNDPYDKLKFVNVDLKEKFSLDLDQYPLGKRFVQAGLRKRP 480
DB 421 FVQSVAILTCQKDAAPAEKNDPYDKLKFVNVDLKEKFSLDLDQYPLGKRFVQAGLRKRP 480
QY 481 IGPKRKSPASATSSKPAKRVVRARK 507
DB 481 IGPKRKSPASATSSKPAKRVVRARK 507

```

RESULT 2
AAB23927 ID AAB23927 standard; protein: 568 AA.

XX AAB23927;

XX 18-JAN-2001 (first entry)

XX Human papillomavirus 18 L1 protein SEQ ID NO:3.

XX Human papillomavirus; HPV16; HPV18; L1 protein; L2 protein; antiviral;
XX vaccine; immunisation; immune response; infection; diagnosis.

OS Human papillomavirus.

XX WO200054730-A2.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US06017.

XX 18-MAR-1999; 99US-0125208.

XX 12-AUG-1999; 99US-0148544.

XX (HARD) HARVARD COLLEGE.

XX (HARR) HARRISON S.

XX (CHEN/) CHEN X.

XX Harrison S, Chen X;

XX WPI; 2000-628165/60.

XX Composition comprising multimer of human papillomavirus L1 protein

XX useful as vaccines against human papillomavirus infection, as

XX diagnostic tools for detecting presence of the virus in biological

XX samples -

XX Disclosure: Page 30; 31pp; English.

XX The present invention describes a composition (I) comprising a multimer

XX of human papillomavirus (HPV) L1 protein (II) which is truncated at its

XX amino terminus. (I) has antiviral activity and can be used in the

XX production of a vaccine. (I) comprising a multimer of HPV L1 protein

XX (a T-1 icosahedral particle comprising a pentamer of L1 protein, one of

XX which comprises HPV L2 protein) when administered induces an immune

XX response against the L1 protein in the humans and is thus useful for

XX immunising the humans against HPV. (I) is thus useful as vaccines against

XX human papillomavirus infection, as diagnostic tools for detecting the

XX presence of HPV in biological samples and as tools for mapping receptor

XX interactions. The present sequence represents an HPV18 L1 protein

XX sequence which is used in the exemplification of the present invention.

XX Sequence 568 AA;

Query Match 99.0%; Score 2705; DB 21; Length 568;
Best Local Similarity 99.0%; Pred. No. 3.8e-247;
Matches 502; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MALMRPSDNTVYLPPPSVAVRVNTDDYVTRTSIFYHAGSSRLTVGNPFYFVPAAGGNKQ 60
DB 62 MALMRPSDNTVYLPPPSVAVRVNTDDYVTRTSIFYHAGSSRLTVGNPFYFVPAAGGNKQ 121
QY 61 DIPVSAVQYVRFVQVLPDPKFKGLPDSIYNPETQRLWMACAGVEIGROPGLGVLSGH 120
DB 122 DIPVSAVQYVRFVQVLPDPKFKGLPDSIYNPETQRLWMACAGVEIGROPGLGVLSGH 181
QY 121 PFYKKLDDTSSHAATSVSEVDVNDVSVYKQIOLCTLGCAPAIGEHMAKGTACKSRPL 180
DB 121 PFYKKLDDTSSHAATSVSEVDVNDVSVYKQIOLCTLGCAPAIGEHMAKGTACKSRPL 180
QY 181 SQGDCPPLLEKNTVLEGDVNDVYTGAMDFSTLQDKCEVPLDQCISCKYPDYLOMSAD 240
DB 242 SQGDCPPLLEKNTVLEGDVNDVYTGAMDFSTLQDKCEVPLDQCISCKYPDYLOMSAD 301
QY 241 PYGDSMFFCLAREDLFAHFNRAGTMDYTPQSLYIKGTGMRASPGSCYVSPSPSGSIV 300
DB 302 PYGDSMFFCLAREDLFAHFNRAGTMDYTPQSLYIKGTGMRASPGSCYVSPSPSGSIV 361
QY 301 TSQSOLFNRKPYWLKKAOGHNNGICMHNOLFVTVVDTTRSTNLITCASQSPVPGQYDATK 360
DB 362 TSQSOLFNRKPYWLKKAOGHNNGICMHNOLFVTVVDTTRSTNLITCASQSPVPGQYDATK 421
QY 361 FKQYSRHVEEYDLOFIQOLCTITLTADVMSYIHSNSSLIEDMNGVPPPTTSLVDTYR 420
DB 422 FKQYSRHVEEYDLOFIQOLCTITLTADVMSYIHSNSSLIEDMNGVPPPTTSLVDTYR 481
QY 421 FVQSVAILTCQKDAAPAEKNDPYDKLKFVNVDLKEKFSLDLDQYPLGKRFVQAGLRKRP 480

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DB      482 FVQSAVITCQKDAAPAEKNDPYDKLKFVWVDLKEKFSLDLDQYPLGRKFLVQAGLRKPT 541
OY      481 IGPKRKSAPSATTSSSKPAKRVRVRARK 507
DB      542 IGPKRKSAPSATTSSSKPAKRVRVRARK 568

RESULT 3
AAB98429
ID      AAB98429 standard; Protein; 568 AA.
AC      AAB98429;
DE      22-AUG-2001 (first entry)
DE      Human papillomavirus protein HPV18 L1.
KM      Human papillomavirus; human leukocyte antigen; HLA; immune response;
KW      HPV; epitope; T cell; identification; vaccine; infection; genital wart;
XX      neoplastic growth; antiviral.
OS      Human papillomavirus.
PN      WO200141799-A1.
PD      14-JUN-2001.
PF      11-DEC-2000; 2000MO-US33549.
PR      10-DEC-1999; 990S-0172705.
PR      15-AUG-2000; 2000DS-0641528.
XX      (EPTM-) EPIMUNE INC.
PI      Setd A, Sidney J, Southwood S, Chesnut R, Cells E, Grey HM;
XX      WPI: 2001-381497/40.
DR      An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT      treating HPV infections -
XX      Disclosure: Page 22; 756pp; English.
PS      The present invention describes an isolated prepared human papillomavirus
CC      (HPV) epitope (I). (I) has antiviral activity, and can be used in
CC      vaccine production. Peptides and corresponding nucleic acid compositions.
CC      from the present invention are useful for stimulating an immune response
CC      to HPV by stimulating the production of CTL or HTL responses,
CC      specifically in the treatment or prophylaxis of HPV infection, in persons
CC      who have not manifested symptoms e.g. genital warts or neoplastic growth.
CC      The peptides can also be used in a tetramer staining assay to assess
CC      peripheral blood mononuclear cells for the presence of antigen-specific
CC      CTLs following exposure to a pathogen or immunogen, and as reagents to
CC      evaluate immune recall responses or evaluate the efficacy of a vaccine.
CC      The vaccine compositions are useful for removing warts or treating HPV
CC      infections. The epitopes for inclusion in an epitope-base vaccine may
CC      be selected from conserved regions of viral or tumour-associated
CC      antigens, which reduces the likelihood of escape mutants, also
CC      immunosuppressive epitopes that may be present in whole antigens can be
CC      avoided with the use of epitope-base vaccines. An additional advantage
CC      is the ability to combine selected epitopes (CTL and HTL) and to modify
CC      the composition of the epitopes achieving enhanced immunogenicity, the
CC      major benefit of the vaccine is that is safe and efficacious. AAB98391
CC      to AAB98477 represent polypeptide sequences used in the exemplification
CC      of the present invention.
SQ      Sequence 568 AA:

```

Query Match 99.0%; Score 2705; DB 22; Length 568;
 Best Local Similarity 99.0%; Pred. No. 3.8e-247;
 Matches 502; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

OY      1 MALMRESDNTVYLPPPSVARVYNTDDYVTRTSIFTHAGSSRLITVGNPFYRVAPAGGNKQ 60
DB      62 MALMRESDNTVYLPPPSVARVYNTDDYVTPTSIFTHAGSSRLITVGNPFYRVAPAGGNKQ 121
OY      61 DIPKVSAYQRYRFRVQLPDPNKFGLPDNSITYPEQRLVMAAGVEIGGQFLGVLGSH 120
DB      122 DIPKVSAYQRYRFRVQLPDPNKFGLPDNSTIYPEQRLVMAAGVEIGGQFLGVLGSH 181
OY      121 PEYNKLDPTRESSHAATSNVEDVRNVSDYKOTOLCIIGCAPAIGEHNAKGTACKSRPL 180
DB      182 PEYNKLDPTRESSHAATSNVEDVRNVSDYKOTOLCIIGCAPAIGEHNAKGTACKSRPL 241
OY      181 SOGDCPPLLEKNTVLEDGDMVDTGAMDFSTLDTKCEVPPLDICSICKYRPTYLQMSAD 240
DB      242 SOGDCPPLLEKNTVLEDGDMVDTGAMDFSTLDTKCEVPPLDICSICKYRPTYLQMSAD 301
OY      241 PYGDSMFCLRRQQLFARHFVNRAGTMDTQSLIKGTGNRASGSCVSPSPSGSTV 300
DB      302 PYGDSMFCLRRQQLFARHFVNRAGTMDTQSLIKGTGNRASGSCVSPSPSGSTV 361
OY      301 TSDSOLFNRPYWLHKAGHNGICWHNQLFVTVVDTRSTNLTICASTOSPVGQYDARK 360
DB      362 TSDSOLFNRPYWLHKAGHNGICWHNQLFVTVVDTRSTNLTICASTOSPVGQYDARK 421
OY      361 FKQYSRHEEYDQLFTQLCTITTLADVMSYIHSNMSILEDWNEGVPPPTSLVDYR 420
DB      422 FKQYSRHEEYDQLFTQLCTITTLADVMSYIHSNMSILEDWNEGVPPPTSLVDYR 481
OY      421 FVQSAVITCQKDAAPAEKNDPYDKLKFVWVDLKEKFSLDLDQYPLGRKFLVQAGLRKPT 480
DB      482 FVQSAVITCQKDAAPAEKNDPYDKLKFVWVDLKEKFSLDLDQYPLGRKFLVQAGLRKPT 541
OY      481 IGPKRKSAPSATTSSSKPAKRVRVRARK 507
DB      542 IGPKRKSAPSATTSSSKPAKRVRVRARK 568

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RESULT 4
AA018098
ID      AA018098 standard; Protein; 500 AA.
AC      AA018098;
DE      13-SEP-2002 (first entry)
DE      HPV type 18 L1 protein mutant encoded by gene l1delatc*.
KM      Human papillomavirus type 18; HPV; cancer; L protein; E protein;
XX      cytostatic; virucide; vaccine; lung; cervix; penis; vulva; anus.
OS      Human papillomavirus type 18.
OS      Synthetic.
PN      DE10059630-A1.
XX      06-JUN-2002.
PD      01-DEC-2000; 2000DE-1059630.
PF      01-DEC-2000; 2000DE-1059630.
PR      01-DEC-2000; 2000DE-1059630.
XX      (MED1-) MEDIGENE AG.
PA      Mueller R, Nieland J, Gabelsberger J, Herbst R;
PI      WPI: 2002-520969/56.
XX      N-PSDB; AAL47486.
DR      Composition for treating and preventing tumors caused by human
PT      papilloma virus 18, contains fusion protein of papilloma virus L and E
XX      proteins, preferably truncated
XX      Disclosure: Page 15-16; 64pp; German.

```

XX		The present invention relates to a composition for preventing or treating
CC	tumours caused by human papillomavirus (HPV) 18, involving at least one	
CC	fusion protein of at least one each of L and E proteins from one or more	
CC	papillomaviruses, and optionally also additives or auxiliaries. The	
CC	composition can be used as a vaccine to treat or prevent carcinoma of the	
CC	lung, cervix, penis, vulva and anus. The present sequence is an HPV	
CC	protein.	
CC		
XX		
SO	Sequence 500 AA;	
	Query Match 98.6%; Score 2694; DB 23; Length 500;	
	Best Local Similarity 99.6%; Pred. No. 3.4e-246;	
	Matches 498; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
OY	1 MALMRSPSNTTYLPPPSAVRVNDDYYTRFSIFPHAGSSRLTVGNRYFRVPAGGKKQ 60	
DB	1 MALMRSPSNTTYLPPPSAVRVNDDYYTRFSIFPHAGSSRLTVGNRYFRVPAGGKKQ 60	
OY	61 DIPKVSAYQYRVEFVQVLPDPNKFGLPDNSIYNPETORLVMACAGYEIGROPVLGSLGH 120	
DB	61 DIPKVSAYQYRVEFVQVLPDPNKFGLPDTSIYNPEFGRLVMACAGYEIRGQPLVGSLGH 120	
OY	121 PFYKKLDITTESSHAATSNVSEEDVDNDVSVDRKQQLCLTGCAPAIGEHWAGTACKSRPL 180	
DB	121 PFYKKLDITTESSHAATSNVSEEDVDNDVSVDRKQQLCLTGCAPAIGEHWAGTACKSRPL 180	
OY	181 SQGDGPPELEKNLYLEDGDMDVDTGAGDFSTLDPTKECEPDLICQSICKYPDYLOMSAD 240	
DB	181 SQGDGPPELEKNLYLEDGDMDVDTGAGDFSTLDPTKECEPDLICQSICKYPDYLOMSAD 240	
OY	241 PYGSMFEFLARREQLFAHFENNRAGTMGVPOSILYIKGTGMRSFGSCVYSPSPSGSIV 300	
DB	241 PYGSMFEFLAREQLFAHFENNRAGTMGVPOSILYIKGTGMRSFGSCVYSPSPSGSIV 300	
OY	301 TSDSQLEFNKPFWLHKAOCHNNGCIMHNOLEFTVVDTSTRMILTICASIQSPVPGGYDATK 360	
DB	301 TSDSQLEFNKPFWLHKAOCHNNGCIMHNOLEFTVVDTSTRMILTICASIQSPVPGGYDATK 360	
OY	361 FKQYSRHVEEYDLOFIQOLCTITTLADVMSYIHSMNSSILEDWNEGVPPPTTSILDVTYR 420	
DB	361 FKQYSRHVEEYDLOFIQOLCTITTLADVMSYIHSMNSSILEDWNEGVPPPTTSILDVTYR 420	
OY	421 FVGSVAITTCOKDAIPAEKKDPYDKLKEMNVDLKEKESLDLOYPLGRREFIVQACLRKRP 480	
DB	421 FVGSVAITTCOKDAIPAEKKDPYDKLKEMNVDLKEKESLDLOYPLGRREFIVQACLRKRP 480	
OY	481 IGPKRKSAPSATTSKPKAKR 500	
DB	481 IGPKRKSAPSATTSKPKAKR 500	
RESULT 5		
AAB98442		
ID	AAB98442 standard; Protein; 536 AA.	
XX		
XX	AAB98442;	
DT	22-AUG-2001 (first entry)	
XX		
DE	Human Papillomavirus protein HPV45 L1.	
KW	Human Papillomavirus; human leukocyte antigen: HLA; immune response;	
KW	HPV; epitope: T cell; identification: vaccine; infection; genital wart;	
KW	neoplastic growth; antiviral.	
OS	Human papillomavirus.	
PN	MO200141799-A1.	
PD	14-JUN-2001.	
PF	11-DEC-2000; 2000OWO-US33549.	

XX	10-DEC-1999; 99US-0172705.
PR	15-AUG-2000; 2000US-0641528.
PA	(EPIM-) EPIMUNE INC.
PI	Sette A, Sidney J, Southwood S, Chesnut R, Cells E, Grey HM;
DR	WPl: 2001-381497/40.
XX	An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT	treating HPV infections -
PS	Disclosure: Page 25; 756pp; English.
XX	
CC	The present invention describes an isolated prepared human papillomavirus
CC	(HPV) epitope (I). (I) has antiviral activity, and can be used in
CC	vaccine production. Peptides and corresponding nucleic acid compositions
CC	from the present invention are useful for stimulating an immune response
CC	to HPV by stimulating the production of CTL or HTL responses,
CC	specifically in the treatment or prophylaxis of HPV infection, in persons
CC	who have not manifested symptoms e.g. genital warts or neoplastic growth.
CC	The peptides can also be used in a tetramer staining assay to assess
CC	peripheral blood mononuclear cells for the presence of antigen-specific
CC	CTLs following exposure to a pathogen or immunogen, and as reagents to
CC	evaluate immune recall responses or evaluate the efficacy of a vaccine.
CC	The vaccine compositions are useful for removing warts or treating HPV
CC	infections. The epitopes for inclusion in an epitope-base vaccine may
CC	be selected from conserved regions of viral or tumour-associated
CC	antigens, which reduces the likelihood of escape mutants, also
CC	immunosuppressive epitopes that may be present in whole antigens can be
CC	avoided with the use of epitope-base vaccines. An additional advantage
CC	is the ability to combine selected epitopes (CTL and HTL) and to modify
CC	the composition of the epitopes achieving enhanced immunogenicity, the
CC	major benefit of the vaccine is that is safe and efficacious. AAB98391
CC	to AAB98477 represent polypeptide sequences used in the exemplification
CC	of the present invention.
XX	
SQ	Sequence 536 AA:
	Query Match 89.9%; Score 2457.5; DB 22; Length 536;
	Best Local Similarity 87.6%; Pred. No. 9.9e-224;
	Matches 447; Conservative 29; Mismatches 31; Indels 3; Gaps 2;
OY	1 MALMRPDSNTVYLPPPSVARYVNDTDVYRTSIFYHAGSSRLTLVGNEYFR-VBAGGKNK 59
DB	::: ::: ::: ::: ::: ::: ::: :::
	27 MALMRPDSSTVYLPPLPPSVARVYVNDTDVYSRFSIFYHAGSSRLTLVGNEYFRVVPVSAGNKK 86
OY	60 ODIPKVASVYQRYRVRYOLPDNNKGFLPNNSLYNETOKLVMAQGVETGRDPLGVGSIG 119
DB	::: ::: ::: ::: ::: ::: ::: :::
	87 QAVRKVASVYQRYRVRYALPDNNKGFLPDLSTIYNPETORLVMAQGMELGRQPLATIGISG 146
OY	120 HPFYNKLDLTDESSHAASTNVSEEDVADVNYVKOTQLCLICAPAIQGHMKAQTACKSRP 179
DB	::: ::: ::: ::: ::: ::: ::: :::
	147 HPEFNKLDDTBSAHAATFAYITQDVADVNSVDYKOTQLCLICAPAIQGHMKAQTCKXQAQ 206
OY	180 LSGQDCPPLLEKNTVLEDGDVADVTGYGAMDSTLDTRCEVPLDICOSICKPYDTLOMSA 239
DB	::: ::: ::: ::: ::: ::: ::: :::
	207 LQPEDCPPLELKNTIIEDGDVADVTGYGAMDFSTLDTRCEVPLDICOSICKPYDTLOMSA 266
OY	240 DPYGDSMFEFCRRROLFAHFHMNRAGTVGDVDPOLSLYKGT--GMRASPSCSYSPSPSG 297
DB	::: ::: ::: ::: ::: ::: ::: :::
	267 DPGYDSMFECRRROLFARHFMNRAGA VGDVDPIDLYIKGISANMKRETPSGCYSPSPSG 326
OY	298 SIYVSDSOLEFKPYWLKRAQGHNNGICWHNOLEVTVVDTSTRNLJTICASTQSPEVPGQYD 357
DB	::: ::: ::: ::: ::: ::: ::: :::
	327 SITTSDSOLFENKPYWLKRAQGNHGNCIHNOLEFTVVADTSTRNLJTICASTQNVPVPTYD 386
OY	358 ATKRKQYSRHHAEEDLOEIPOLCITTLADVMASYHSNNSILDMNMGVPRPPTLSYD 417
DB	::: ::: ::: ::: ::: ::: ::: :::
	387 PTKRNHISRHEEYDLOEIFOLCTITLLAEWMSTIHSKNSSILEMNMGVPPPTLSYD 446
OY	418 TYRFVQSAVLTCQADAAPAEKNKDVEDYDKLFENNVDLKEKFSIDLDOYPLGRFRFLVQAQARR 477

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Db      447 TTFVSVAVTCCKDPTPEKODPYDKLFWYDLKEKSSDDQYPLGKRLVQGLRR 506
      478 KPTIGPKRRSAPSATSSKPAKRVRRAR 507
      507 RPTIGPKRRPMASTASRAKRVIRSKK 536

RESULT 6
AAB98454
ID      AAB98454 standard; Protein; 534 AA.
AC      AAB98454;
DT      22-AUG-2001 (first entry)
DE      Human papillomavirus protein HPV56 L1.
KW      Human papillomavirus; human leukocyte antigen; HLA; immune response;
KW      HPV; epitope; T cell; identification; vaccine; infection; genital wart;
KW      neoplastic growth; antiviral.
OS      Human papillomavirus.
PN      WO200141799-A1.
PD      14-JUN-2001.
PF      11-DEC-2000; 2000MO-US33549.
PR      10-DEC-1999; 990US-0172705.
PR      15-AUG-2000; 2000US-0641528.
XX      (EPI-M-) EPIMMUNE INC.
PI      Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;
DR      WPI; 2001-381497/40.
PT      An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT      treating HPV infections -
XX      Disclosure; Page 27; 756pp; English.
XX      The present invention describes an isolated prepared human papillomavirus
CC      (HPV) epitope (I). (I) has antiviral activity, and can be used in
CC      vaccine production. Peptides and corresponding nucleic acid compositions
CC      from the present invention are useful for stimulating an immune response
CC      to HPV by stimulating the production of CTL or HTL responses,
CC      specifically in the treatment or prophylaxis of HPV infection, in persons
CC      who have not manifested symptoms e.g. genital warts or neoplastic growth.
CC      The peptides can also be used in a tetramer staining assay to assess
CC      peripheral blood mononuclear cells for the presence of antigen-specific
CC      CTLs following exposure to a pathogen or immunogen, and as reagents to
CC      evaluate immune recall responses or evaluate the efficacy of a vaccine.
CC      The vaccine compositions are useful for removing warts or treating HPV
CC      infections. The epitopes for inclusion in an epitope-based vaccine may
CC      be selected from conserved regions of viral or tumour-associated
CC      antigens, which reduces the likelihood of escape mutants, also
CC      immunosuppressive epitopes that may be present in whole antigens can be
CC      avoided with the use of epitope-based vaccines. An additional advantage
CC      is the ability to combine selected epitopes (CTL and HTL) and to modify
CC      the composition of the epitopes achieving enhanced immunogenicity, the
CC      major benefit of the vaccine is that is safe and efficacious. AAB98391
CC      to AAB98477 represent polypeptide sequences used in the exemplification
CC      of the present invention.
XX      Sequence 534 AA:

```

Query Match 67.7%; Score 1851; DB 22; Length 534;
 Best Local Similarity 67.0%; Pred. No. 3.1e-166;
 Matches 337; Conservative 71; Mismatches 89; Indels 6; Gaps 4;

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QY      1 MALRPSDNTVYLPPPSVAHVNTDDVYTRTSIFYHAGSSRLTLTGPNPYRVPAGGAK 60
      36 MATWRSEKNTVYLPPTFVSKVATDSYKRTSIFYHAGSSRLLAHVHPYSV-TKDNTRY 94
QY      61 DIRKVSAYQYRVFRVQVLPDPNKGFLPONSITYNEQTQLVWACAGVELGKRGQVGLSGH 120
      95 NIPKVSAYQYRVFRVRLPDPNKGFLPNTNINPDQERLVWACVGLGKRGQVGLSGH 154
QY      121 PFYKLLDPTSSSHAATSNVSEEDVADNVSYDKOTQCLICAPAGCHMAKGTACKSRPL 180
      155 PLFNRLDDPTSSNANNVIEDSRDNI SVGKOTQCLIVGCTPAMGSHMKAGVCKSTQV 214
QY      181 SQGDCPPELKNVTLEDGMDVDTGYGAMDESTLQDFKCEVPLDICOSICKPYDLOMSAD 240
      215 TTGDCPPLALINPIEDGMDIDFGAMDEFKVLQESKAEVPLDIVGCTCKPYDLKMSAD 274
QY      241 PYGDSMFPCRLRQLFARHFNWNRAGTMDVPOSLYIKGCGMARSPSCYSSPSGSIV 300
      275 AYGDSMWFYLRRLQFLARHFNWNRAGTMDVPOSLYIKGCGMARSPSCYSSPSGSIV 334
QY      301 TSDSOLENRPYWLHKAQHNNGICWHNQLFVTVVDTFRSTNLTICASTQSPVGOYDAFK 360
      335 TSEAOLEFNKPYWLQRAQGHNGICWHNQLFVTVVDTFRSTNLTICASTQSPVGOYDAFK 392
Db      361 FQYSRHVEEYDLOFQLOCTITLTDVMSYIHSNMSILEDNMFVPPPTSLVDTRY 420
      393 INQYLRHVEEYDLOFQLOCTITLTDVMSYIHSNMSILEDNMFVPPPTSLVDTRY 452
QY      421 FVOSVAITCOKDAAPAKNKPYDKLKWVNDLKEKSLDDOYPLGKRLVQAGLRKPT 480
      453 YVRSATATCQREOPPTKOPPLAKYKFWVDNLDSFSTDIDQPLGKRLVQAGLRKPT 512
QY      481 IG-PRKRSAPSATSSKPAKRV 502
      513 VATSKRSAP--ISTSTPAKRRK 533
Db

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RESULT 7
AAB98436
ID      AAB98436 standard; Protein; 504 AA.
AC      AAB98436;
DT      22-AUG-2001 (first entry)
DE      Human papillomavirus protein HPV31 L1.
KW      Human papillomavirus; human leukocyte antigen; HLA; immune response;
KW      HPV; epitope; T cell; identification; vaccine; infection; genital wart;
KW      neoplastic growth; antiviral.
OS      Human papillomavirus.
PN      WO200141799-A1.
PD      14-JUN-2001.
PF      11-DEC-2000; 2000MO-US33549.
PR      10-DEC-1999; 990US-0172705.
PR      15-AUG-2000; 2000US-0641528.
XX      (EPI-M-) EPIMMUNE INC.
PI      Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;
DR      WPI; 2001-381497/40.
PT      An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT      treating HPV infections -
XX      Disclosure; Page 23-24; 756pp; English.
XX

```

CC The present invention describes an isolated prepared human papillomavirus
 CC (HPV) epitope (I). (I) has antiviral activity, and can be used in
 CC vaccine production. Peptides and corresponding nucleic acid compositions
 CC from the present invention are useful for stimulating an immune response
 CC to HPV by stimulating the production of CTL or HTL responses.
 CC Specifically in the treatment or prophylaxis of HPV infection, in persons
 CC who have not manifested symptoms e.g. genital warts or neoplastic growth.
 CC The peptides can also be used in a tetramer staining assay to assess
 CC peripheral blood mononuclear cells for the presence of antigen-specific
 CC T cells following exposure to a pathogen or immunogen, and as reagents to
 CC evaluate immune recall responses or evaluate the efficacy of a vaccine.
 CC The vaccine compositions are useful for removing warts or treating HPV
 CC infections. The epitopes for inclusion in an epitope-base vaccine may
 CC be selected from conserved regions of viral or tumour-associated
 CC antigens, which reduces the likelihood of escape mutants, also
 CC immunosuppressive epitopes that may be present in whole antigens can be
 CC avoided with the use of epitope-base vaccines. An additional advantage
 CC is the ability to combine selected epitopes (CTL and HTL) and to modify
 CC the composition of the epitopes achieving enhanced immunogenicity, the
 CC major benefit of the vaccine is that is safe and efficacious. AAB98391
 CC to AAB98477 represent polypeptide sequences used in the exemplification
 CC of the present invention.

XX Sequence 504 AA:

Query Match 67.1%; Score 1834.5; DB 22; Length 504;
 Best Local Similarity 65.1%; Pred. No. 1e-164;
 Matches 329; Conservative 79; Mismatches 94; Indels 3; Gaps 3;

QY 1 MALNRPSNTYVYLLPPPSARVYNTDDYTRTSISYFHAGSSRLTYGNGFYRVPAGGKQ 60
 DB 1 MSIMRPSATYVYLLPPPSARVYNTDDYTRTSISYFHAGSSRLTYGNGFYRVPAGGKQ 60
 QY 61 -DIPKVSAYQYVFRVQLDPNKFGLPNSIYVPEQRLVWACAGVEIGRQPLVGLSG 119
 DB 61 IYVPEVSGIYQYVFRVQLDPNKFGLPNSIYVPEQRLVWACAGVEIGRQPLVGLSG 120
 QY 120 HPFNKLDDESSHAATSNVSEVDVNDVYKOTQCLICGAPRIGHMAKGTACKSRP 179
 DB 121 HPFNKLDDESSHAATSNVSEVDVNDVYKOTQCLICGAPRIGHMAKGTACKSRP 180
 QY 180 LSGDCPPLLELKNVYLEDGDMVDYTGAMDEFTLDTCCEVPLDTCOSICRYPDLOMSA 239
 DB 181 ITPDCPPLLELKNVYLEDGDMVDYTGAMDEFTLDTCCEVPLDTCOSICRYPDLOMSA 240
 QY 240 DPGDSMFCLRRQLEFARHFWNRAGTMDVYPOSILYIKGTGMRASPCSCVYSPSPSGSI 299
 DB 241 EPGDTLFEYLRREQMEFARHFWNRAGTMDVYPOSILYIKGTGMRASPCSCVYSPSPSGSI 300
 QY 300 VTSOSLEFNKRYWHLHKGHNNGICWNLQFLVYVDTFRSTNLTCATOSPVREQYDAT 359
 DB 301 VTSOSLEFNKRYWHLHKGHNNGICWNLQFLVYVDTFRSTNLTCATOSPVREQYDAT 359
 QY 360 KFKOYSRHEVEYDLOFIFOLCTITLADVMSYIHSNMSISLEDNMFVPPPTSLVPTY 419
 DB 360 NFKELRIRGEFEDLOFIFOLCTITLADVMSYIHSNMSISLEDNMFVPPPTSLVPTY 419
 QY 420 RFVOSVAITCOKDAAPAKNDPYDKLFWNDLKEKESLDIQYPLGKFTLVQAGLRKP 479
 DB 420 RFVOSVAITCOKDAAPAKNDPYDKLFWNDLKEKESLDIQYPLGKFTLVQAGLRKP 479
 QY 480 TIGPRKRSAPSATSSRKARVRYR 504
 DB 480 KFKAGKRSAPSATSSRKARVRYR 504

RESULT 8
 AAB75800
 ID AAB75800 standard; Protein: 505 AA.
 XX AAB75800;
 AC
 XX 08-MAY-2003 (first entry)
 DT

XX Human papillomavirus 16 L1 protein, clone p114/16/11.
 DE
 XX HPV16: virus-like particle; VLP; infection; cancer; tumour; L1;
 KW anogenital tract; uterine cervix; clone p114/16/11; virucide; vaccine.
 KM
 XX Human papillomavirus 16.
 OS
 XX US2002168372-A1.
 PN
 XX 14-NOV-2002.
 PD
 XX 29-SEP-1998; 98US-0162904.
 PF
 XX 16-JUL-1993; 93US-0092528.
 PR 01-MAY-1996; 96US-0641570.
 PR 27-JUN-1997; 97US-0884168.
 XX
 PA (DURS/) DURST M.
 PA (GISS/) GISSMANN L.
 PI
 XX Durst M, Gissmann L;
 XX
 DR WPI: 2003-275319/27.
 DR N-PSDB: ABB11396.
 XX
 PT New DNA sequence encoding an L1 protein of a papillomavirus capable of
 PT forming virus-like particles, useful for preparing a vaccine against
 PT papillomavirus infection, particularly human papillomavirus (HPV)16
 PT infection
 PS Disclosure: Fig 2; 17pp; English.

XX The invention discloses a DNA sequence encoding an L1 protein of a human
 CC papillomavirus (HPV16) capable of forming virus-like particles (VLPs).
 CC Papillomaviruses infections have been linked to malignant cancer and
 CC malignant tumours of the anogenital tract, particularly cancer of the
 CC uterine cervix. Also disclosed is an antibody that is specifically
 CC directed against the VLP or the L1 protein, a method for determining
 CC anti-HPV16 virion antibodies in a sample and prophylaxis of
 CC papillomavirus infections. The DNA sequence is useful for preparing a
 CC vaccine against papillomavirus infection, particularly HPV16 infection.
 CC The DNA is used to produce a VLP which can be used in a diagnostic kit
 CC to determine anti-HPV16 virion antibodies of papillomavirus infections and the DNA
 CC used to produce an L1 protein. The sequence presented is the HPV16 L1
 CC protein, clone p114/16/11.
 CC
 XX

SO Sequence 505 AA:

Query Match 67.0%; Score 1831; DB 24; Length 505;
 Best Local Similarity 66.5%; Pred. No. 2.2e-164;
 Matches 334; Conservative 68; Mismatches 96; Indels 4; Gaps 3;

QY 1 MALNRPSNTYVYLLPPPSARVYNTDDYTRTSISYFHAGSSRLTYGNGFYRVPAGGKQ 60
 DB 1 MSIMRPSATYVYLLPPPSARVYNTDDYTRTSISYFHAGSSRLTYGNGFYRVPAGGKQ 60
 QY 61 -DIPKVSAYQYVFRVQLDPNKFGLPNSIYVPEQRLVWACAGVEIGRQPLVGLSG 120
 DB 61 IYVPEVSGIYQYVFRVQLDPNKFGLPNSIYVPEQRLVWACAGVEIGRQPLVGLSG 120
 QY 120 HPFNKLDDESSHAATSNVSEVDVNDVYKOTQCLICGAPRIGHMAKGTACKSRP 179
 DB 121 HPFNKLDDESSHAATSNVSEVDVNDVYKOTQCLICGAPRIGHMAKGTACKSRP 180
 QY 180 LSGDCPPLLELKNVYLEDGDMVDYTGAMDEFTLDTCCEVPLDTCOSICRYPDLOMSA 239
 DB 181 ITPDCPPLLELKNVYLEDGDMVDYTGAMDEFTLDTCCEVPLDTCOSICRYPDLOMSA 240
 QY 240 DPGDSMFCLRRQLEFARHFWNRAGTMDVYPOSILYIKGTGMRASPCSCVYSPSPSGSI 299
 DB 241 EPGDTLFEYLRREQMEFARHFWNRAGTMDVYPOSILYIKGTGMRASPCSCVYSPSPSGSI 300
 QY 300 VTSOSLEFNKRYWHLHKGHNNGICWNLQFLVYVDTFRSTNLTCATOSPVREQYDAT 359
 DB 301 VTSOSLEFNKRYWHLHKGHNNGICWNLQFLVYVDTFRSTNLTCATOSPVREQYDAT 359
 QY 360 KFKOYSRHEVEYDLOFIFOLCTITLADVMSYIHSNMSISLEDNMFVPPPTSLVPTY 419
 DB 360 NFKELRIRGEFEDLOFIFOLCTITLADVMSYIHSNMSISLEDNMFVPPPTSLVPTY 419
 QY 420 RFVOSVAITCOKDAAPAKNDPYDKLFWNDLKEKESLDIQYPLGKFTLVQAGLRKP 479
 DB 420 RFVOSVAITCOKDAAPAKNDPYDKLFWNDLKEKESLDIQYPLGKFTLVQAGLRKP 479
 QY 480 TIGPRKRSAPSATSSRKARVRYR 504
 DB 480 KFKAGKRSAPSATSSRKARVRYR 504

QY 301 TSDSOLFNRPYWLHKAQGHNNGICWGNOLFVYVDTTRSTNLTICASTOSPVVGQYDARK 360
 DB 301 TSDAOLFNRPYWLHKAQGHNNGICWGNOLFVYVDTTRSTNLTICAAI-STSETTKNTN 359
 QY 361 FKQYSHRVEEYDLOFIFOLCTITLTDVNSYIHSNSSLIEDMNFVPPPTSLVDYR 420
 DB 360 FKQYSHRVEEYDLOFIFOLCTITLTDVNSYIHSNSSLIEDMNFVPPPTSLVDYR 419
 QY 421 FVQSAITQCKDAAPAKENKDPYDKLFVWVNDLKEKESLDDOYPLGRKFLVQAGLRKP- 479
 DB 420 FVTSQAIAQCKHPPAPKEDPLKKYTFWEVNLKEKESADLDOPPLGRKFLVQAGLRKP 479
 QY 480 -TIGPKRRSAPSATSSKPAKR 500
 DB 480 FTIGKRR-ATPTSTSTTAKR 500

RESULT 9
 AAY08019
 ID AAY08019 standard; Protein; 505 AA.
 AC AAY08019;
 XX
 DT 08-JUL-1999 (first entry)
 XX
 DE Human papilloma virus L1 protein.
 XX
 KM L1 protein; capsomer; virus; vaccine; infection; treatment; prevention;
 KM cervical carcinoma; fusion protein; anti-capsid; antibody;
 KM antigenicity.
 XX
 OS Human papilloma virus.
 XX
 PN W09918220-A1.
 PD 15-APR-1999.
 XX
 PF 06-OCT-1998; 98WO-US20965.
 XX
 PR 06-OCT-1997; 97US-0944368.
 XX
 PA (LOYO) UNIV LOYOLA CHICAGO.
 XX
 PI Gissmann L, Mueller M;
 DR WPI; 1999-264026/22.
 DR N-PSDB; AAX37566.
 XX
 PT Human papilloma virus (HPV) L1 fusion protein capsomers, used in
 XX vaccines against HPV infection
 PS
 PS Disclosure; Page 31-32; 48pp; English.
 XX
 CC This invention describes novel vaccines comprising a human papilloma
 CC virus (HPV) capsomer, composed of a HPV L1 fusion protein or a HPV L1
 CC truncated protein. The vaccines can prevent or treat human papilloma
 CC virus infection. Such therapeutic vaccinations can be used for relief
 CC against, e.g. cervical carcinoma. Construction of chimeric proteins
 CC comprising amino acid residues from L1 protein, and e.g. E6 or E7
 CC protein, which give rise to chimeric capsomers, combines prophylactic and
 CC therapeutic functions of a vaccine. Capsomers can promote elimination of
 CC persistently infected cells. Capsomers can also escape neutralization
 CC by pre-existing anti-capsid antibodies and hence possess longer
 CC circulating half-life as compared to chimeric virus-like particles.
 CC The fusion protein, which forms the capsomer, provides increased
 CC antigenicity.
 CC
 SQ Sequence 505 AA;

Query Match 66.8%; Score 1826; DB 20; Length 505;
 Best Local Similarity 66.3%; Pred. No. 6 6e-164;
 Matches 333; Conservative 68; Mismatches 97; Indels 4; Gaps 3;

QY 1 MALMRSDNTVYLLPPESVARVNTDDYVETSTIFYHAGSSRLTLVGNPFYRVPAGGNKO 60
 DB 1 MSMLPSEANVYLLPPVPSKSVSTDEYVARTNIYHAGSRLLAVGHPPFIKKPNMKI 60
 QY 61 DIPKVSAYQRYRFRVLPDPNKFGLPDNSIYNDETQRLVWACGVEIRGQPLGVLGSH 120
 DB 61 LVPKVSGLQRYRFRVLPDPNKFGLPDNSIYNDETQRLVWACGVEIRGQPLGVLGSH 120
 QY 121 PFNKTLDPTSSHAASNSSEVDVAVSVYKOTOLCIGCAPAIGEHAKGTACKSRPL 180
 DB 121 PLNKTLDPTSSHAASNSSEVDVAVSVYKOTOLCIGCAPAIGEHAKGTACKSRPL 180
 QY 181 SGGDCPPLLEKNTVLEDDGMVDTGYGAMPFSTLDTKCEVPLDICOICKPYLQMSAD 240
 DB 181 NPDCPPLLEKNTVLEDDGMVDTGYGAMPFSTLDTKCEVPLDICOICKPYLQMSAD 240
 QY 241 PYGDSMEFCLRRQLEFARHFWNRAQMGDTVPQSLYIKGTGRASPSCVSPSGSIY 300
 DB 241 PYGDSMEFCLRRQLEFARHFWNRAQMGDTVPQSLYIKGTGRASPSCVSPSGSIY 300
 QY 301 TSDSOLFNRPYWLHKAQGHNNGICWGNOLFVYVDTTRSTNLTICASTOSPVVGQYDARK 360
 DB 301 TSDAOLFNRPYWLHKAQGHNNGICWGNOLFVYVDTTRSTNLTICAAI-STSETTKNTN 359
 QY 361 FKQYSHRVEEYDLOFIFOLCTITLTDVNSYIHSNSSLIEDMNFVPPPTSLVDYR 420
 DB 360 FKQYSHRVEEYDLOFIFOLCTITLTDVNSYIHSNSSLIEDMNFVPPPTSLVDYR 419
 QY 421 FVQSAITQCKDAAPAKENKDPYDKLFVWVNDLKEKESLDDOYPLGRKFLVQAGLRKP- 479
 DB 420 FVTSQAIAQCKHPPAPKEDPLKKYTFWEVNLKEKESADLDOPPLGRKFLVQAGLRKP 479
 QY 480 -TIGPKRRSAPSATSSKPAKR 500
 DB 480 FTIGKRR-ATPTSTSTTAKR 500

RESULT 10
 AAY57720
 ID AAY57720 standard; Protein; 505 AA.
 AC AAY57720;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Human papillomavirus L1 fusion protein SEQ ID NO:2.
 XX
 KM Human papillomavirus; HPV; L1 fusion protein; vaccine; cytostatic;
 KM viral capsomere; virucide; dermatological; malignant tumour formation;
 KM condylomata acuminata.
 XX
 OS Human papillomavirus.
 OS Synthetic.
 XX
 PN CA2229955-A1.
 PD 20-AUG-1999.
 XX
 PF 20-FEB-1998; 98CA-2229955.
 XX
 PR 20-FEB-1998; 98CA-2229955.
 XX
 PA (MED-) MEDIGENE GMBH.
 XX
 PI Burger A, Hallek M;
 DR WPI; 2000-063092/06.
 DR N-PSDB; AAZ48174.
 XX
 PT Fusion proteins comprising papillomavirus specific proteins useful for
 vaccinating against malignant tumors of the anogenital tract such as

[illegible]

Db	241	PYGDSLEFFYLRRQOMFRRHLFNRAGAVGENVPDDLYIGSGSTANLASSNYFFTPSGSMV	3001
Oy	301	TTSQSOLEFNKPYWLHKRQGNHNGICWHNOLFVYVVDYTTSTLTLTCASTQSGVPRQDAYTK	360
Db	301	TTSQAOLEFNKPYWLQKQGNHNGICWGNOLFVYVVDYTTSTLTKNSLCAAI-STSETTYKNTN	359
Oy	361	FKQSYHVEEYDQLEFQCTTTLTADVASYIHSNNSILDDMNFVGPPEPTTSLVDYTR	420
Db	360	FKREYLHNGEYDQLEFQCTTTLTADVATYIHSNNSITLEDNMFGLOPPGGTLEDTYR	419
Oy	421	FVQSVATLTCOKDAAPENKDPYDKLFEMVNDLKEKESLDDQYPLGRKFVQAGLRKRP	479
Db	420	FVTSQALACOKHPPAPKEDPLKTYFMEVNLKEKESADLDQPLGRKFLLQAGLRKAPK	479
Oy	480	-TIGPRKRSAPSATSSSKPAKR 500	
Db	480	FTLGKRR-ATPTTSTSTTAKR 500	
RESULT 13			
AAB98422			
ID	AAB98422	standard; Protein; 531 AA.	
XX	AAB98422;		
XX			
XX	22-AUG-2001	(first entry)	
XX			
DE		Human papillomavirus protein HPV16 L1.	
XX			
XX		Human papillomavirus; human leukocyte antigen; HLA; Immune response;	
KW	HPV; epitope; T cell; identification; vaccine; infection; genital wart;		
KW	neoplastic growth; antiviral.		
OS			
XX	Human papillomavirus.		
FN	MO20014179-A1.		
XX			
PD	14-JUN-2001.		
XX			
PF	11-DEC-2000; 2000MO-US33549.		
XX			
PR	10-DEC-1999; 99US-0172705.		
PR	15-AUG-2000; 2000US-0641528.		
XX			
PA	(EPIM-) EPIMUNE INC.		
XX			
PI	Sette A, Sidney J, Southwood S, Chesnut R, Cells E, Grey HM;		
XX	WPI; 2001-381497/40.		
DR			
XX			
PT	An isolated human papilloma virus (HPV) epitope, useful in vaccines for		
XX	treating HPV infections -		
PS	Disclosure; Page 21; 756pp; English.		
XX			
CC	The present invention describes an isolated prepared human papillomavirus		
CC	(HPV) epitope (1). (1) has antiviral activity, and can be used in		
CC	vaccine production. Peptides and corresponding nucleic acid compositions		
CC	from the present invention are useful for stimulating an immune response		
CC	to HPV by stimulating the production of CTL or HTL responses, im-		
CC	specifically in the treatment or prophylaxis of HPV infection, in persons		
CC	who have not manifested symptoms e.g. genital warts or neoplastic growth.		
CC	The peptides can also be used in a tetramer staining assay to assess		
CC	peripheral blood mononuclear cells for the presence of antigen-specific		
CC	CTLs following exposure to a pathogen or immunogen, and as reagents to		
CC	evaluate immune recall responses or evaluate the efficacy of a vaccine.		
CC	The vaccine compositions are useful for removing warts or treating HPV		
CC	infections. The epitopes for inclusion in an epitope-base vaccine may		
CC	be selected from conserved regions of viral or tumour-associated		
CC	antigens, which reduces the likelihood of escape mutants, also		
CC	immunosuppressive epitopes that may be present in whole antigens can be		
CC	avoided with the use of epitope-base vaccines. An additional advantage		


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RESULT 15
AA38807
ID AAR38807 standard; Protein; 505 AA.
XX
AC AAR38807;
XX
DT 25-MAR-2003 (updated)
DT 17-DEC-2001 (updated)
DT 21-JAN-1994 (first entry)
XX
DE BPV1 L1.
XX
KW L1; capsid protein; bovine; human; papillomavirus; baculovirus;
KW transfer vector; promoter; capsid protein; transformation; vaccine;
KW neutralising antibody; vertebrate.
XX
OS Bovine papillomavirus.
XX
PN USN8032869-N.
XX
PD 15-JUL-1993.
XX
PF 16-MAR-1993; 93US-0032869.
XX
PR 03-SEP-1992; 92US-0941371.
XX
PR 16-MAR-1993; 93US-0032869.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX
PI Kirnbauer R, Lowy DR, Schiller JT;
XX
DR WPI; 1993-249995/31.
XX
DR N-PSDB; AAQ47166.
XX
PT Recombinant papilloma virus capsid proteins - for vaccines
PT against papilloma virus and for diagnosis of virus infection
XX
PS Example 1; Page 32-34; 45pp; English.
XX
CC The sequences given in AAR38807-08 represent the L1 capsid proteins from
CC bovine and human papillomavirus respectively. The DNA encoding these
CC sequences may be inserted into a baculovirus transfer vector and
CC operatively expressed by a promoter of the vector, and the capsid
CC protein produced by transformed cells. These capsid proteins may be
CC used in vaccines to induce high-titre neutralising antibody response
CC in vertebrates.
CC (Note: Revised entry submitted to correct the patent number format of
CC US Government-owned NTIS applications to prevent clashes with ongoing US
CC granted patent numbers. For further information please visit the Derwent
CC web site at www.derwent.com/dwpi/updates/ntis-us.html.)
CC
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 505 AA;
QY
Query Match 66.7%; Score 1824; DB 14; Length 505;
Best Local Similarity 66.3%; Pred. No. 1e-163;
Matches 333; Conservative 68; Mismatches 97; Indels 4; Gaps 3;
Db 1 MALMRSDMTVYILPPSVARVYVTDYVTRTSIFYHAGSSRLITVGNPFYFRVAGGQNK 60
1 MSLLPSEATVYILPPVPSKVVSTDEYVARTNIIYHAGTSRLAVGHPYPIKPPNNNKI 60
QY 61 DIPKSAVQYRVFVQLPDPNKGFLPDNSIYNPETQRLVWACAGVEIGRQPLGVLSGH 120
61 IVPKVSGLQYRVFRIHLDPNKGFLPDJTSFYNDIQLVWACAGVEIGRQPLGVLSGH 120
Db 61 IVPKVSGLQYRVFRIHLDPNKGFLPDJTSFYNDIQLVWACAGVEIGRQPLGVLSGH 120
QY 121 PFYNNKLDITRESSHAATSNVSEVDYNDVSDYKQTOQLICGAPADIGEHWAKGTACKSRPL 180
121 PFYNNKLDITRESSHAATSNVSEVDYNDVSDYKQTOQLICGAPADIGEHWAKGTACKSRPL 180
Db 121 PLTNKLDITRENSAVYANAGVDNRECIISMDYKQTOQLICGKPIGEHWKGSPTCNVAV 180
121 PLTNKLDITRENSAVYANAGVDNRECIISMDYKQTOQLICGKPIGEHWKGSPTCNVAV 180
QY 181 SGGDCPPLLEKNTVLEDDGMVDVGYGAMDFSTLQDTKCPPLDICSICKYPPDYLMNSAD 240
181 SGGDCPPLLEKNTVLEDDGMVDVGYGAMDFSTLQDTKCPPLDICSICKYPPDYLMNSAD 240

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Db 181 NPGDCPPLLELINTVYIODGDMVHTFGAMDETTIQAANKSEVPLDICTSICKYPPDYIMVSE 240
QY 241 PYGDSMEFCLRRQLEFARHFWRNAGTMDVTPQSLYIKGTGMRASPGSCYSPSGSIY 300
241 PYGDSMEFCLRRQLEFARHFWRNAGTMDVTPQSLYIKGTGMRASPGSCYSPSGSIY 300
Db 241 PYGDSMEFCLRRQLEFARHFWRNAGTMDVTPQSLYIKGTGMRASPGSCYSPSGSIY 300
QY 301 TSDSQLEFNKPYWLHKAQGNNGICWHNQLEFVTVVDTTRSTNLTICASTQSPVPGQYDARK 360
301 TSDSQLEFNKPYWLHKAQGNNGICWHNQLEFVTVVDTTRSTNLTICASTQSPVPGQYDARK 360
Db 301 TSDSQLEFNKPYWLHKAQGNNGICWHNQLEFVTVVDTTRSTNLTICASTQSPVPGQYDARK 360
QY 361 FKQYSRHVEEYDLOFIFOLCTITLTDVMSYHSMNSSTLEDNMFVPPPTSLVDYR 420
361 FKQYSRHVEEYDLOFIFOLCTITLTDVMSYHSMNSSTLEDNMFVPPPTSLVDYR 420
Db 361 FKQYSRHVEEYDLOFIFOLCTITLTDVMSYHSMNSSTLEDNMFVPPPTSLVDYR 420
QY 421 FVQSVAITCQKDAAPAKENKDPYDLKFWNDLKEKESLIDQYPLGKRFVQGLRRKP- 479
421 FVQSVAITCQKDAAPAKENKDPYDLKFWNDLKEKESLIDQYPLGKRFVQGLRRKP- 479
Db 420 FVQSVAITCQKDAAPAKENKDPYDLKFWNDLKEKESLIDQYPLGKRFVQGLRRKP- 479
QY 480 -TIGPKRRSAPSAATSSKPAKR 500
480 -TIGPKRRSAPSAATSSKPAKR 500
Db 480 -TIGPKRRSAPSAATSSKPAKR 500

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Search completed: October 17, 2003, 10:59:07
Job time : 64.8512 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 17, 2003, 10:47:38 ; Search time 15.7128 seconds
(without alignments)
1517.395 Million cell updates/sec

Title: US-08-913-644-2

Perfect score: 2733
Sequence: 1 MALMRPSDNTVYLPPSVAR.....APSATTSSKPKRRVRARRK 507

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2705	99.0	568	VL1_HPV18	P06794 human papill
2	2450	89.6	539	VL1_HPV45	P36741 human papill
3	2179.5	79.7	504	VL1_HPV70	P50793 human papill
4	2155	78.9	505	VL1_HPVME	P27964 human papill
5	2151	78.7	505	VL1_HPV39	P24838 human papill
6	2141	78.3	505	VL1_HPV68	P54669 human papill
7	1956	71.6	503	VL1_HPV29	P50792 human papill
8	1917.5	70.2	532	VL1_HPV03	P36731 human papill
9	1912.5	70.0	502	VL1_HPV28	P50791 human papill
10	1909	69.8	531	VL1_HPV10	P36732 human papill
11	1879	68.8	508	VL1_HPV30	P02515 human papill
12	1861.5	68.1	503	VL1_HPV26	P36735 human papill
13	1855.5	67.9	505	VL1_HPV61	P50892 human papill
14	1855	67.9	499	VL1_HPV53	P05113 human papill
15	1855	67.9	501	VL1_HPV1	P22163 rhesus papill
16	1851	67.7	534	VL1_HPV56	P36743 human papill
17	1837	67.2	497	VL1_HPV54	P50819 human papill
18	1834.5	67.1	504	VL1_HPV31	P17388 human papill
19	1822	66.7	503	VL1_HPV66	P080961 human papill
20	1820.5	66.6	502	VL1_HPV35	P27222 human papill
21	1804.5	66.0	504	VL1_HPV51	P26536 human papill
22	1804.5	66.0	524	VL1_HPV58	P26535 human papill
23	1801.5	65.9	529	VL1_HPV52	P05138 human papill
24	1801	65.9	531	VL1_HPV16	P03101 human papill
25	1791	65.5	499	VL1_HPV33	P06416 human papill
26	1789.5	65.5	510	VL1_HPV2A	P25466 human papill
27	1784.5	65.2	510	VL1_HPV2	P22162 human papill
28	1781	65.2	502	VL1_HPV1	P02274 pygmy chipm
29	1771	64.8	594	VL1_HPV27	P36736 human papill
30	1771	64.8	505	VL1_HPV07	P05136 human papill
31	1768.5	64.7	500	VL1_HPV6A	P03100 human papill
32	1766	64.6	505	VL1_HPV40	P36740 human papill
33	1763	64.5	528	VL1_HPV34	P36738 human papill

34	1762	64.5	503	VL1_HPV32	P36737 human papill
35	1759	64.4	499	VL1_HPV13	P02273 human papill
36	1757	64.3	502	VL1_HPV42	P27233 human papill
37	1751.5	64.1	501	VL1_HPV55	P50820 human papill
38	1745	63.8	500	VL1_HPV44	P50816 human papill
39	1733	63.4	501	VL1_HPV11	P04012 human papill
40	1427	52.2	514	VL1_HPV08	P06417 human papill
41	1426.5	52.2	546	VL1_HPV19	P02050 human papill
42	1426	52.2	516	VL1_HPV20	P50786 human papill
43	1425.5	52.2	517	VL1_HPV12	P36736 human papill
44	1422.5	52.0	517	VL1_HPV25	P02051 human papill
45	1421	52.0	510	VL1_HPV38	P50814 human papill

ALIGNMENTS

```

RESULT 1
VL1_HPV18 STANDARD; PRT; 568 AA.
AC P06794; 084270;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Major capsid protein L1.
GN L1.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87283882; PubMed=3039146;
RA Cole S.T., Danos O.;
RT "Nucleotide sequence and comparative analysis of the human
RT papillomavirus type 18 genome. Phylogeny of papillomaviruses and
RT repeated structure of the E6 and E7 gene products."
RL J. Mol. Biol. 193:599-608(1987).
RN [2]
RP SEQUENCE OF 363-406 FROM N.A.
RX MEDLINE=92407963; PubMed=1326639;
RA Chan S.Y., Bernard H.U., Ong C.K., Chan S.P., Birgit H., Delius H.;
RT "Phylogenetic analysis of 48 papillomavirus types and 28 subtypes and
RT variants: a showcase for the molecular evolution of DNA viruses."
RL J. Virol. 66:5714-5725(1992).
RN [3]
RP SEQUENCE OF 501-568 FROM N.A.
RX MEDLINE=87061231; PubMed=3023691;
RA Thierry F., Heard J.M., Dartmann K., Yaniv M.;
RT "Characterization of a transcriptional promoter of human
RT papillomavirus 18 and modulation of its expression by simian virus 40
RT and adenovirus early antigens."
RL J. Virol. 61:134-142(1987).
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-----
DR EMBL: X05015; CA28671.1; -
DR EMBL: M96287; AAA47026.1; -
DR EMBL: M14710; AAA65508.1; -
DR EMBL: A06329; CA00545.1; -
DR PIR: A26251; P1WL18.
DR InterPro: IPR002210; PV_capsid.L1.
DR Pfam: PF00500; late_protein.L1.
DR PRINTS: PR00865; HPVcapsid.L1.
DR ProDom: PD000544; PV_capsid.L1.
DR CoaT protein: Late protein.
KW CONFLICT 384 384 V -> I (IN REF. 2).

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SQ SEQUENCE 568 AA: 63623 MW: BB2BF361177FC10 CRC64:
 Query Match 99.0%; Score 2705; DB 1; Length 568;
 Best Local Similarity 99.0%; Pred. No. 8.7e-227;
 Matches 502; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MALMRPSNTYLLPPPSVARYVNDYTRTSIFTHAGSSRLTYGNPFYRPVAGGKQ 60
 DB 62 MALMRPSNTYLLPPPSVARYVNDYTRTSIFTHAGSSRLTYGNPFYRPVAGGKQ 121
 QY 61 DIPKVSAYQYRVFVQVLPDPNKGFLPDSINYPETQRLVWACAGVEIGRQPLGVLGSH 120
 DB 122 DIPKVSAYQYRVFVQVLPDPNKGFLPDSINYPETQRLVWACAGVEIGRQPLGVLGSH 181
 QY 121 PFYNNKLDTESSHAATSNVSEVDVNDVSKQVQLCICGAPALGEHMAKGTACKSRPL 180
 DB 182 PFYNNKLDTESSHAATSNVSEVDVNDVSKQVQLCICGAPALGEHMAKGTACKSRPL 241
 QY 181 SGGDCPRLKNTYLEDDGMVDYTGAMDESTLDOTKCEVPLDQCSICKYPTDYLQMSA 240
 DB 242 SGGDCPRLKNTYLEDDGMVDYTGAMDESTLDOTKCEVPLDQCSICKYPTDYLQMSA 301
 QY 241 PYGDSMFECLRRQDLFAHFNNRAGTMDYVPOSILYIKGTGMRASPGSCVSPSPSGSIV 300
 DB 302 PYGDSMFECLRRQDLFAHFNNRAGTMDYVPOSILYIKGTGMRASPGSCVSPSPSGSIV 361
 QY 301 TSDSOLFENKPYMLHKAQGHNGICWNHOLFVTVVDTTRSTNLITLCASQSPVPGQYDAK 360
 DB 362 TSDSOLFENKPYMLHKAQGHNGICWNHOLFVTVVDTTRSTNLITLCASQSPVPGQYDAK 421
 QY 361 FKQSRHVEEYDLOFIFOLCTITTLADYMSYIHSNSSLIDMNGVPPPTSLVDYR 420
 DB 422 FKQSRHVEEYDLOFIFOLCTITTLADYMSYIHSNSSLIDMNGVPPPTSLVDYR 481
 QY 421 FVQSVATTCQKDAAPAEKNDYDKLFKNVNDLKEKFSLDLDQYPLGRKFLVQAQGLRRPT 480
 DB 482 FVQSVATTCQKDAAPAEKNDYDKLFKNVNDLKEKFSLDLDQYPLGRKFLVQAQGLRRPT 541
 QY 481 IGPKRKRSAPATSSKPAKRVRRARK 507
 DB 542 IGPKRKRSAPATSSKPAKRVRRARK 568
 RESULT 2
 VIL_HPV45 STANDARD; PRT; 539 AA.
 ID VIL_HPV45
 AC P36741;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Major capsid protein LI.
 GN LI.
 OS Human papillomavirus type 45.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 CC Papillomavirus.
 OX NCBI_TaxID=10593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94265501; PubMed=8205838;
 RA Delius H., Hofmann B.;
 RT "Primer-directed sequencing of human papillomavirus types";
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
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 CC -----
 DR EMBL: X74479; CAAS2578.1; -
 DR PIR: S36566; S36566.

DR InterPro: IPR002210; PV_capsid_L1.
 DR Pfam: PF00500; late_protein_L1; 1.
 DR PRINTS: PR00865; HPVcapsidL1.
 DR Prodom: PD000544; PV_capsid_L1; 1.
 KW Coat protein; late protein.
 SQ SEQUENCE 539 AA: 60310 MW: 9D79F6804234E5E CRC64:
 Query Match 89.6%; Score 2450; DB 1; Length 539;
 Best Local Similarity 87.3%; Pred. No. 1.1e-204;
 Matches 448; Conservative 30; Mismatches 29; Indels 6; Gaps 3;
 QY 1 MALMRPSNTYLLPPPSVARYVNDYTRTSIFTHAGSSRLTYGNPFYRPVAGGK 59
 DB 27 MALMRPSNTYLLPPPSVARYVNDYTRTSIFTHAGSSRLTYGNPFYRPVAGGK 86
 QY 60 DIPKVSAYQYRVFVQVLPDPNKGFLPDSINYPETQRLVWACAGVEIGRQPLGVLGSH 119
 DB 87 DIPKVSAYQYRVFVQVLPDPNKGFLPDSINYPETQRLVWACAGVEIGRQPLGVLGSH 146
 QY 120 HPFYNNKLDTESSHAATSNVSEVDVNDVSKQVQLCICGAPALGEHMAKGTACKSRP 179
 DB 147 HPFYNNKLDTESSHAATSNVSEVDVNDVSKQVQLCICGAPALGEHMAKGTACKSRP 206
 QY 180 LSOGDCPRLKNTYLEDDGMVDYTGAMDESTLDOTKCEVPLDQCSICKYPTDYLQMSA 239
 DB 207 LSOGDCPRLKNTYLEDDGMVDYTGAMDESTLDOTKCEVPLDQCSICKYPTDYLQMSA 266
 QY 240 PYGDSMFECLRRQDLFAHFNNRAGTMDYVPOSILYIKGT - GMRASPGSCVSPSPSG 297
 DB 267 PYGDSMFECLRRQDLFAHFNNRAGTMDYVPOSILYIKGT - GMRASPGSCVSPSPSG 326
 QY 298 STVSDSOLFENKPYMLHKAQGHNGICWNHOLFVTVVDTTRSTNLITLCASQSPVPGQYD 357
 DB 327 STVSDSOLFENKPYMLHKAQGHNGICWNHOLFVTVVDTTRSTNLITLCASQSPVPGQYD 386
 QY 358 ATKQSRHVEEYDLOFIFOLCTITTLADYMSYIHSNSSLIDMNGVPPPTSLVDY 417
 DB 387 ATKQSRHVEEYDLOFIFOLCTITTLADYMSYIHSNSSLIDMNGVPPPTSLVDY 446
 QY 418 TYRFVQSVATTCQKDAAPAEKNDYDKLFKNVNDLKEKFSLDLDQYPLGRKFLVQAQGLRR 477
 DB 447 TYRFVQSVATTCQKDAAPAEKNDYDKLFKNVNDLKEKFSLDLDQYPLGRKFLVQAQGLRR 506
 QY 478 KPTIGPKRRKAPD--ATTSSKPAKRVRRARK 507
 DB 507 KPTIGPKRRKAPD--ATTSSKPAKRVRRARK 539
 RESULT 3
 VIL_HPV70 STANDARD; PRT; 504 AA.
 ID VIL_HPV70
 AC P50793;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Major capsid protein LI.
 GN LI.
 OS Human papillomavirus type 70.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 CC Papillomavirus.
 OX NCBI_TaxID=39457;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96249586; PubMed=8815087;
 RA Forslund O., Hansson B.G.;
 RT "Human papillomavirus type 70 genome cloned from overlapping PCR
 RT products: complete nucleotide sequence and genomic organization";
 RL J. Clin. Microbiol. 34:802-809(1996).
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 CC -----
 DR EMBL: X74479; CAAS2578.1; -
 DR PIR: S36566; S36566.

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RT related to the potentially oncogenic HPV39."
RL J. Clin. Microbiol. 34:738-744(1996).
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CC -----
DR EMBL: U21941; AAC54857.1; -
DR EMBL: U22461; AAC54879.1; -
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1; 1.
DR PRINTS: PR00865; HPVcapsidL1.
DR ProDom: PD000544; PV_capsid_L1; 1.
DR Coat protein; late protein.
KW CONFLICT 39 39 S -> T (IN REF. 2).
FT CONFLICT 178 178 T -> TTV (IN REF. 2).
SQ SEQUENCE 504 AA; 56576 MW; 0E9029B5B3F3DC5 CRC64;

Query Match
Best Local Similarity 79.7%; Score 2179.5; DB 1; Length 504;
Matches 393; Conservative 50; Mismatches 61; Indels 3; Gaps 2;

QY 1 MALMRSDNTVYLPPPSVAVVNTDDYVTRTSIFTHAGSSRLTVGNPFYRVAGGKQ 60
DB 1 MALMRSDNTVYLPPPSVAVVNTDDYVTRTSIFTHAGSSRLTVGNPFYRVAGGKQ 60
QY 61 DIPKVSAYQYRVFRVQLPDPNKGFLPDNSIYNDETQRLVWACGVEIGRGQPLGVLGSH 120
DB 61 DIPKVSAYQYRVFRVQLPDPNKGFLPDNSIYNDETQRLVWACGVEIGRGQPLGVLGSH 120
QY 121 PFYNRKLDDESSHAASNSYEDVRDVSVDYKOTQCTICIGCAPAIGEHNAKAGACKSRPL 180
DB 121 PFYNRKLDDESSHAASNSYEDVRDVSVDYKOTQCTICIGCAPAIGEHNAKAGACKSRPL 180
QY 121 PLYNRLDDESSHAASNSYEDVRDVSVDYKOTQCTICIGCAPAIGEHNAKAGACKSRPL 180
DB 121 PLYNRLDDESSHAASNSYEDVRDVSVDYKOTQCTICIGCAPAIGEHNAKAGACKSRPL 180
QY 181 SOGDCPPELKTNYLEDGDMVDYGYGAMDFSTLDKCEVPLDICKSICKYPPDYLOMSAD 240
DB 179 OGDGCPPELKTNYLEDGDMVDYGYGAMDFSTLDKCEVPLDICKSICKYPPDYLOMSAD 238
QY 241 PYGDSMFCLRRQLEFARHFNWAGTGMGTVPQSLYIKGTGMARASGSCVSPSPSGSIY 300
DB 239 YGDSMFCLRRQLEFARHFNWAGTGMGTVPQSLYIKGTGMARASGSCVSPSPSGSIY 298
QY 301 TSDSOLFENKPYWLHKAQGNNGICWNOLEFVVDTRSTNLTICASTOSPVPQGYDARK 360
DB 299 SSDSOLFENKPYWLHKAQGNNGICWNOLEFVVDTRSTNLTICASTOSPVPQGYDARK 358
QY 361 FKQYSHVEEYDQLEFQCTITLTFADVNSYIHSNNSILEDPMNFGVPPPTSLVDYTR 420
DB 359 FKQYSHVEEYDQLEFQCTITLTFADVNSYIHSNNSILEDPMNFGVPPPTSLVDYTR 418
QY 421 FVQSAITQCQKDAAPARENDDPYDKLFWMVNDLKEKFSLLDQYPLGRKFLVQAGLRKPT 480
DB 419 YLQSAITQCQKDAAPARENDDPYDKLFWMVNDLKEKFSLLDQYPLGRKFLVQAGLRKPT 478
QY 481 IGPRKRSAPATSSSKPAKRVRRAR 507
DB 479 IGPRKRSAPATSSSKPAKRVRRAR 504

RESULT 4
VIL_HPVME
ID VIL_HPVME STANDARD; PRT; 505 AA.
AC P27964;
DR 01-AUG-1992 (rel. 23, Created)
DR 01-AUG-1992 (rel. 23, Last sequence update)
DR 16-OCT-2001 (rel. 40, Last annotation update)
DE Major capsid protein L1.
GN L1.
OS Human papillomavirus type ME180.

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OC viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374616; PubMed=1716694;
RA Reuter S., Deltus H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;
RT "Characterization of a novel human papillomavirus DNA in the cervical
RL carcinoma cell line ME180."
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CC -----
DR EMBL: M73258; AAF14010.1; -
DR PIR: B40509; P1MLPR.
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1; 1.
DR PRINTS: PR00865; HPVcapsidL1.
DR ProDom: PD000544; PV_capsid_L1; 1.
DR Coat protein; late protein.
KW SEQUENCE 505 AA; 56805 MW; 595DE493B708207B CRC64;

Query Match
Best Local Similarity 78.9%; Score 2155; DB 1; Length 505;
Matches 386; Conservative 52; Mismatches 65; Indels 0; Gaps 0;

QY 1 MALMRSDNTVYLPPPSVAVVNTDDYVTRTSIFTHAGSSRLTVGNPFYRVAGGKQ 60
DB 1 MALMRSDNTVYLPPPSVAVVNTDDYVTRTSIFTHAGSSRLTVGNPFYRVAGGKQ 60
QY 61 DIPKVSAYQYRVFRVQLPDPNKGFLPDNSIYNDETQRLVWACGVEIGRGQPLGVLGSH 120
DB 61 DIPKVSAYQYRVFRVQLPDPNKGFLPDNSIYNDETQRLVWACGVEIGRGQPLGVLGSH 120
QY 121 PFYNRKLDDESSHAASNSYEDVRDVSVDYKOTQCTICIGCAPAIGEHNAKAGACKSRPL 180
DB 121 PFYNRKLDDESSHAASNSYEDVRDVSVDYKOTQCTICIGCAPAIGEHNAKAGACKSRPL 180
QY 121 PLYNRLDDESSHAASNSYEDVRDVSVDYKOTQCTICIGCAPAIGEHNAKAGACKSRPL 180
DB 121 PLYNRLDDESSHAASNSYEDVRDVSVDYKOTQCTICIGCAPAIGEHNAKAGACKSRPL 180
QY 181 SOGDCPPELKTNYLEDGDMVDYGYGAMDFSTLDKCEVPLDICKSICKYPPDYLOMSAD 240
DB 181 OGDGCPPELKTNYLEDGDMVDYGYGAMDFSTLDKCEVPLDICKSICKYPPDYLOMSAD 240
QY 241 PYGDSMFCLRRQLEFARHFNWAGTGMGTVPQSLYIKGTGMARASGSCVSPSPSGSIY 300
DB 241 PYGDSMFCLRRQLEFARHFNWAGTGMGTVPQSLYIKGTGMARASGSCVSPSPSGSIY 300
QY 301 TSDSOLFENKPYWLHKAQGNNGICWNOLEFVVDTRSTNLTICASTOSPVPQGYDARK 360
DB 301 SSDSOLFENKPYWLHKAQGNNGICWNOLEFVVDTRSTNLTICASTOSPVPQGYDARK 360
QY 361 FKQYSHVEEYDQLEFQCTITLTFADVNSYIHSNNSILEDPMNFGVPPPTSLVDYTR 420
DB 359 FKQYSHVEEYDQLEFQCTITLTFADVNSYIHSNNSILEDPMNFGVPPPTSLVDYTR 420
QY 421 FVQSAITQCQKDAAPARENDDPYDKLFWMVNDLKEKFSLLDQYPLGRKFLVQAGLRKPT 480
DB 421 YLQSAITQCQKDAAPARENDDPYDKLFWMVNDLKEKFSLLDQYPLGRKFLVQAGLRKPT 480
QY 481 IGPRKRSAPATSSSKPAKRVRRAR 503
DB 481 IGPRKRSAPATSSSKPAKRVRRAR 503

RESULT 5
VIL_HPV39
ID VIL_HPV39 STANDARD; PRT; 505 AA.
AC P24838;

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DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Major capsid protein L1.
GN L1.
OS Human papillomavirus type 39.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_Taxid=10588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9135017; PubMed=1847266;
RA Volpers C., Streck R.E.;
RT "Genome organization and nucleotide sequence of human papillomavirus
type 39."
RL Virology 181:419-423(1991).
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DR EMBL: M62849; AAA47056.1; -
DR PIR: H38502; P1MW39.
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1; 1.
DR PRINTS: PR00865; HPVcapsidL1.
DR ProDom: PD000544; PV_capsid_L1; 1.
KM Coat protein: late protein.
SQ SEQUENCE 505 AA; 56604 MW; 73854F9F1C56BCD CRC64;

Query Match 78.7%; Score 2151; DB 1; Length 505;
Best Local Similarity 77.3%; Pred. No. 8.6e-179;
Matches 391; Conservative 48; Mismatches 61; Indels 6; Gaps 3;

QY 1 MALTSPSDNVTYLPPEPVAVRYNTDVTYRTSIFHAAGSSRLTVGNPFRVPAAGGKQ 60
DB 1 MAMRSBDSMYLPPPPVAKVNTDDVTYTRGIYVAGSSRLTVGHPYFVGMNGGKQ 60
QY 61 DIPVSAIYQYRVFVLPDPNKKFGLPDNSIYNPETORLWMAAGVEIGRGQPLGVLSGH 120
DB 61 DIPVSAIYQYRVFVLPDPNKKFGLPDNSIYNPETORLWMAAGVEIGRGQPLGVLSGH 120
QY 121 PFYKRLDTESSHAATSNVSEVDVNVSVYKQTOQLICCAPAIGEHMAKGTACKSRPL 180
DB 121 PFYKRLDTESSHAATSNVSEVDVNVSVYKQTOQLICCAPAIGEHMAKGTACKSRPL 180
QY 121 PLYNRQDTESSHAATSNVSEVDVNVSVYKQTOQLICCAPAIGEHMAKGTACKSRPL 179
DB 121 PLYNRQDTESSHAATSNVSEVDVNVSVYKQTOQLICCAPAIGEHMAKGTACKSRPL 179
QY 181 SOGCPPELEKNTYLEGDMVDYGYGANDSTLQDTKCEVPLDLCOSICKPYLYQMSAD 240
DB 181 SOGCPPELEKNTYLEGDMVDYGYGANDSTLQDTKCEVPLDLCOSICKPYLYQMSAD 240
QY 180 STGCAPPELEKNTYLEGDMVDYGYGANDSTLQDTKCEVPLDLCOSICKPYLYQMSAD 239
DB 180 STGCAPPELEKNTYLEGDMVDYGYGANDSTLQDTKCEVPLDLCOSICKPYLYQMSAD 239
QY 241 PYGDSMEFCLAREDLFAHFNWNRAGTMDVYPOSILYKGTGMASPSGCVSPSPSGSIY 300
DB 241 PYGDSMEFCLAREDLFAHFNWNRAGTMDVYPOSILYKGTGMASPSGCVSPSPSGSIY 300
QY 240 VYGDSEMFCLAREDLFAHFNWNRAGTMDVYPOSILYKGTGMASPSGCVSPSPSGSIY 299
DB 240 VYGDSEMFCLAREDLFAHFNWNRAGTMDVYPOSILYKGTGMASPSGCVSPSPSGSIY 299
QY 301 TSDSOLFENKPYWLKKAAGHNGICMHNQLFVTVVDTTRSTNLITCASTQSPVPGQYDATK 360
DB 301 TSDSOLFENKPYWLKKAAGHNGICMHNQLFVTVVDTTRSTNLITCASTQSPVPGQYDATK 360
QY 300 TSDSOLFENKPYWLKKAAGHNGICMHNQLFVTVVDTTRSTNLITCASTQSPVPGQYDATK 359
DB 300 TSDSOLFENKPYWLKKAAGHNGICMHNQLFVTVVDTTRSTNLITCASTQSPVPGQYDATK 359
QY 361 FKQYSRHVEEDLQFIQOLCTITLTADVMSTIHSNSSLIEDNMGVPPPTTSVLYDTYR 420
DB 361 FKQYSRHVEEDLQFIQOLCTITLTADVMSTIHSNSSLIEDNMGVPPPTTSVLYDTYR 420
QY 360 FKQYSRHVEEDLQFIQOLCTITLTADVMSTIHSNSSLIEDNMGVPPPTTSVLYDTYR 419
DB 360 FKQYSRHVEEDLQFIQOLCTITLTADVMSTIHSNSSLIEDNMGVPPPTTSVLYDTYR 419
QY 421 FYGSAVATTCQKDAAPAKNKDYPDKLKFVNVDLKEKFSLDLQYPLGKRFVQGLRRKPT 480
DB 421 FYGSAVATTCQKDAAPAKNKDYPDKLKFVNVDLKEKFSLDLQYPLGKRFVQGLRRKPT 480
QY 481 IGPKRSPASATSSKPA--KRVAV 503
DB 481 IGPKRSPASATSSKPA--KRVAV 503
QY 480 IGPKR--PAASTSSSATKHKRRV 503
DB 480 IGPKR--PAASTSSSATKHKRRV 503
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RESULT 6
VLI_HPV68 STANDARD; PRT; 505 AA.
AC P54669;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Major capsid protein L1.
GN L1.
OS Human papillomavirus type 68.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_Taxid=45240;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97060129; PubMed=8904450;
RA Longuet M., Beaudenon S., Orth G.;
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,
RL J. Clin. Microbiol. 34:738-744(1996).
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DR EMBL: X67161; CAA47634.1; -
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1; 1.
DR PRINTS: PR00865; HPVcapsidL1.
DR ProDom: PD000544; PV_capsid_L1; 1.
KM Coat protein: late protein.
SQ SEQUENCE 505 AA; 56693 MW; 246CDB4DAB2A1997 CRC64;

Query Match 78.3%; Score 2141; DB 1; Length 505;
Best Local Similarity 75.9%; Pred. No. 6.4e-178;
Matches 382; Conservative 56; Mismatches 65; Indels 0; Gaps 0;

QY 1 MALTSPSDNVTYLPPEPVAVRYNTDVTYRTSIFHAAGSSRLTVGNPFRVPAAGGKQ 60
DB 1 MAMRSBDSMYLPPPPVAKVNTDDVTYTRGIYVAGSSRLTVGHPYFVGMNGGKQ 60
QY 61 DIPVSAIYQYRVFVLPDPNKKFGLPDNSIYNPETORLWMAAGVEIGRGQPLGVLSGH 120
DB 61 DIPVSAIYQYRVFVLPDPNKKFGLPDNSIYNPETORLWMAAGVEIGRGQPLGVLSGH 120
QY 121 PFYKRLDTESSHAATSNVSEVDVNVSVYKQTOQLICCAPAIGEHMAKGTACKSRPL 180
DB 121 PFYKRLDTESSHAATSNVSEVDVNVSVYKQTOQLICCAPAIGEHMAKGTACKSRPL 180
QY 121 PLYNRQDTESSHAATSNVSEVDVNVSVYKQTOQLICCAPAIGEHMAKGTACKSRPT 180
DB 121 PLYNRQDTESSHAATSNVSEVDVNVSVYKQTOQLICCAPAIGEHMAKGTACKSRPT 180
QY 181 SOGCPPELEKNTYLEGDMVDYGYGANDSTLQDTKCEVPLDLCOSICKPYLYQMSAD 240
DB 181 SOGCPPELEKNTYLEGDMVDYGYGANDSTLQDTKCEVPLDLCOSICKPYLYQMSAD 240
QY 180 STGCAPPELEKNTYLEGDMVDYGYGANDSTLQDTKCEVPLDLCOSICKPYLYQMSAD 239
DB 180 STGCAPPELEKNTYLEGDMVDYGYGANDSTLQDTKCEVPLDLCOSICKPYLYQMSAD 239
QY 241 PYGDSMEFCLAREDLFAHFNWNRAGTMDVYPOSILYKGTGMASPSGCVSPSPSGSIY 300
DB 241 PYGDSMEFCLAREDLFAHFNWNRAGTMDVYPOSILYKGTGMASPSGCVSPSPSGSIY 300
QY 240 VYGDSEMFCLAREDLFAHFNWNRAGTMDVYPOSILYKGTGMASPSGCVSPSPSGSIY 300
DB 240 VYGDSEMFCLAREDLFAHFNWNRAGTMDVYPOSILYKGTGMASPSGCVSPSPSGSIY 300
QY 301 TSDSOLFENKPYWLKKAAGHNGICMHNQLFVTVVDTTRSTNLITCASTQSPVPGQYDATK 360
DB 301 TSDSOLFENKPYWLKKAAGHNGICMHNQLFVTVVDTTRSTNLITCASTQSPVPGQYDATK 360
QY 300 TSDSOLFENKPYWLKKAAGHNGICMHNQLFVTVVDTTRSTNLITCASTQSPVPGQYDATK 359
DB 300 TSDSOLFENKPYWLKKAAGHNGICMHNQLFVTVVDTTRSTNLITCASTQSPVPGQYDATK 359
QY 361 FKQYSRHVEEDLQFIQOLCTITLTADVMSTIHSNSSLIEDNMGVPPPTTSVLYDTYR 420
DB 361 FKQYSRHVEEDLQFIQOLCTITLTADVMSTIHSNSSLIEDNMGVPPPTTSVLYDTYR 420
QY 360 FKQYSRHVEEDLQFIQOLCTITLTADVMSTIHSNSSLIEDNMGVPPPTTSVLYDTYR 419
DB 360 FKQYSRHVEEDLQFIQOLCTITLTADVMSTIHSNSSLIEDNMGVPPPTTSVLYDTYR 419
QY 421 FYGSAVATTCQKDAAPAKNKDYPDKLKFVNVDLKEKFSLDLQYPLGKRFVQGLRRKPT 480
DB 421 FYGSAVATTCQKDAAPAKNKDYPDKLKFVNVDLKEKFSLDLQYPLGKRFVQGLRRKPT 480
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Dh      421 YLQSAATTCQADAPAPVKKDDPYDGINFENVNLKEKFSSELDQFLGRNFLAQAGRRRRT 480
Qy      481 IGPKRKSAPASATTSSKPAKRVY 503
         |||||.: :||: | |
Db      481 IGPKRRTATATTSTSKHKRRV 503

RESULT 7
V_L1_HPV29 STANDARD; PRT; 503 AA.
ID V_L1_HPV29 AC P50792;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE Major capsid protein L1.
GN L1.
OS Human papillomavirus type 29.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=371112;
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/Genbank/DDBJ databases.
RN [2]
RP SEQUENCE OF 316-467 FROM N.A.
RX MEDLINE=95052821; PubMed=796396;
RA Bernard H.U., Chan S.Y., Manos M.M., Ong C.K., Villa L.L.,
RA Delius H., Peyton C.L., Bauer H.M., Wheeler C.M.;
RT "Identification and assessment of known and novel human
RT papillomaviruses by polymerase chain reaction amplification,
RT restriction fragment length polymorphisms, nucleotide sequence, and
RT phylogenetic algorithms."
RT J. Infect. Dis. 170:1077-1085(1994).
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DR EMBL; U31784; AAA79435.1; -.
DR EMBL; U12503; AAA67247.1; -.
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00805; late_protein_L1; 1.
DR PRINTS; PR00865; HPVcapsidL1.
DR ProDom: PD000544; PV_capsid_L1; 1.
DR KCoat protein; Late protein.
DR KW SEQUENCE 503 AA; 56281 MW; 8D2E36DAABD30847 CRC64;

Query Match          71.6%; Score 1956; DB 1; Length 503;
Best Local Similarity 69.3%; Pred. No.7.le-162;
Matches 348; Conservative 70; Mismatches 82; Indels 2; Gaps 1

Qy      1 MALMRPSDMTYLPDPSPVARVYNTDDYTSTSYFYHAGSSRLTLTGNYFFRYPAGGAKKO 60
         ||||| :||| ||||| :||: :||:|||||:|||||:|||||:| :||
Db      1 MALMRSSDNLYLPDPPTPKYSKVISTDDYTTRINITYAASSRLTLTVGHHSIPKSGNKV 60

Qy      61 DIPVVSAYQIVYERFOLDPNKKFGILPDNSITNPETQRLLVMACAGVEIGRGOPLVGLSGH 120
         |:|||||:|||||:|||||:||||| :||| :|||||:|||||:|||||
Db      61 DVPRVSASFQYVFYFRRLRDLPPDKFKGLPDARIYNPEARLYMVACTGVYGRGQPLVGLSGH 120

Qy      121 PFYRKLDPTESHSHATSNVSDVDVRNVSVDVKQQQLCLTGCAPARAGEHMAKTACKSRPL 180
         | :|||:||||:| :| :| :|||:|||||:|||||:||||| :||| |||
Db      121 PLTKKLNDTENSNTLAHAENGDSNRNIADVKKQQLCLTGCTPPGHEHGKGTVCARTSS 180

Qy      181 SQGGCPPLELTENLYLEDDAMVDTEGGADEFSLDTCKCEVPDLICOSICKYDYLOMSAD 240
         : :|||:| | :|||:|||||:|||||:| :| :|||:| | :|
Db      181 AAGCGCPPLEMTHTIHEDGDMDVTGEGANDPALQYKNKSDVPLDICQSICKYDIYGMAAD 240

Qy      241 PYGDSMFECFLRRQLFAHFHNWNAQTGMDTPQSLYLIRGTGMRASPSCSVSPSPSGSIV 300

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Db      241  P Y G S M F E L R R E D L F A R H F N R A G V G D K I P D S L Y L K G N N G R E P T P S A I T S P P S G S M V
QY      301  T S D S L F N K P Y W L T L K A G H N N G I C M H N Q L E F Y V D T R S T N L T C A S T O S P V P G O Y A T K
Db      301  T S E A Q I N K P Y W L Q A G H N N G I C M A Q V E L T V Y D T R S T N M S L C A T T E S O P L T T Y A T K
QY      361  F K O Y S R H V E E Y D L F I O L C T T L T P A D V M S Y I H S M S S I L E D N M F G V P P P T S L Y D T Y R
Db      421  F V Q S V A L T C Q K D A P A E N K P D Y D L K A W N V D L A K K E S L I D D Y L F G R K F L Y O A G L R K K P T
QY      421  F V T S S A T T C C K D A L P T E K O P Y A K I N F W D V L D K D R F L D I S Q F L G R K F L I O I G A R R S V
Db      481  I G P R K S A P S A T T S S K P A R V R 502
QY      481  V P S K R R R - T T T A P T P A K R R R 500

RESULT 8
VL1_HPV03
AC      P36731. STANDARD; PRT; 532 AA.
ID      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      01-OCT-1996 (Rel. 34, Last annotation update)
DE      Major capsid protein L1.
GN      L1
OS      Human papillomavirus type 3.
OC      Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      Papillomavirus.
OX      NCBI_TaxID=10614;
[1]
RP      SEQUENCE FROM N.A.
FX      MEDLINE=94265501; PubMed=8205838;
RA      Delius H., Hofmann B.;
RT      "Primer-directed sequencing of human papillomavirus types 3,
RL      Curr. Top. Microbiol. Immunol. 186:13-31(1994).
[1]
CC      -1- CAVUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-29 IS THE INITIATOR.
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DR      EMBL; X74462; CAAS2474.1; -
DR      PIR; S36554; S36554.
DR      InterPro: IPR002210; PV_capsid_L1.
DR      Pfam: PF00500; late_protein_L1; 1.
DR      PRINTS; PR00865; HPV_CAPSID_L1.
DR      ProDom; PD000544; PV_capsid_L1; 1.
KW      Coat protein; Late protein.
SQ      SEQUENCE 532 AA; 59194 MW; A0AFB87DBEE98B27 CRC64;

Query Match 70.2%; Score 1917.5; DB 1; Length 532;
Best Local Similarity 68.8%; Pred. No. 17/e-158;
Matches 351; Conservative 65; Mismatches 85; Indels 9; Gaps 4;

QY      1  M A L R P S D N M Y L P P S P V A R V N D D V Y T R T S I F Y H A G S S R L L V G N D P Y P R V A P G G N K Q 60
Db      29  M A L M R S S D N L Y L P P T P V S K V L S D D Y T R T N I T Y I Y A G S S L L V G H P F A I P R S S N S K M 88

QY      61  D I P V K S A Y O Y R V F E V O L P D P N K F G L P N S I Y I N P T O R L I W A C A G E L I G R G O P L A G S G H 120
Db      89  D I P V S A F O Y R V F E V R L P D P N K F G L P A R I T N P A E K L V A C I G V E V G R G L P L G V G S G H 148

QY      121  P F Y K L D D T E S S H A A T S N S E D V D N V S V D I K O T O L C I L G A P A I G E H M A K T A C K S R P L 180
Db      149  P L Y K K L D D T E S S I N A H D I G K D S D N I S V D N K O T O L I V G C T P P M G E H M G S G F C K O N - A 207

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QY 181 SGGDCPELEKNTVLEDGMDVDTGYGAMDESTLDPTKCEVPLDICSICKPYDYLQMSAD 240
 Db 208 SPGCPPELEITAPIDGMDVDTGYGAMDEGNLSNKSVDPLDICTCKKPYDYLQMAAE 267
 QY 241 PYGDSMEFCLRRQDLFARHFWNRAGTMDVPOSlyTKG---TCMRASPSGCVYSPSPSG 297
 Db 268 PYGDSMEFCLRRQDLFARHFWNRAGTMDVPOSlyTKGSGSGRKGISAVYCPSPSG 327
 QY 298 SIYSDSOLEFNKPYWLHKAQGNHNGICWNOLEFVTVDTSTNTLTICASTQSPVPGQYD 357
 Db 328 SMVTSSEQLFNKPYWLHKAQGNHNGICWNOLEFVTVDTSTNTLTICASTQSPVPGQYD 385
 QY 358 ATFKQYSRVEEDLQFIQOLCTITLTADVASTIHSNSSLIEDMNFVPPPTSLVD 417
 Db 386 ATFKEXLRGEEYDQFIQOLCKVTLTPEIMAYLHTMNSTLLEDNMFGLTLPSTSLIED 445
 QY 418 TYRVSQVATTCOKDAPPAENKDPYDKLFKFWNVDLKKEFSLLDQYLRGRFLVQAQLRR 477
 Db 446 TYRFLTSALTTCOKDAPPTKEDPYAKLNFMDVDLKRFSLDLSQFPLGRKFLMQLGVGT 505
 QY 478 KPTIGPKRSAPSATYSSSKPAKRVYRARK 507
 Db 506 RSSISVYKR--SATTSSTPAAKAKRKRTKK 532

RESULT 9

VL1_HPV28 STANDARD; PRF: 502 AA.

ID VL1_HPV28

AC P50791;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Major capsid protein L1.

GN L1.

OS Human papillomavirus type 28.

OC Viruses; dsDNA viruses, no RNA stage: Papillomaviridae;

OC Papillomavirus.

OX NCBI_Taxid=37111;

RN [1]

RP SEQUENCE FROM N.A.

RA Delius H.;

RT Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 316-464 FROM N.A.

RX MEDLINE=95052821; Pubmed=7963696;

RA Bernard H.U., Chan S.Y., Manos M.M., Ong C.K., Villa L.L.,

RT Delius H., Peyton C.L., Bauer H.M., Wheeler C.M.;

RT "Identification and assessment of known and novel human

RT papillomaviruses by polymerase chain reaction amplification,

RT restriction fragment length polymorphisms, nucleotide sequence, and

RT phylogenetic algorithms."

RT J. Infect. Dis. 170:1077-1085(1994).

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CC EMBL: U31783; AAA79428.1; -

DR EMBL: U12502; AAA67246.1; -

DR InterPro: IPR002210; PV_capsid.L1.

DR Pfam: PF00500; late_protein.L1; 1.

DR PRINTS: PR00865; HPVcapsid.L1.

DR PRODOM: PD000544; PV_capsid.L1; 1.

KW Coat protein; Late protein.

SQ SEQUENCE 502 AA; 55902 MW; 38D6EADBI2AF310A CRC64;

Query Match 70.0%; Score 1912.5; DB 1; Length 502;

Best Local Similarity 68.3%; Pred. No. 4.2e-158;

Matches 345; Conservative 70; Mismatches 85; Indels 5; Gaps 4;
 QY 1 MALMRPSDNTVYLPPEPSVAHVNTDYVYTSIFTHAGSSRLTVGNPYRVAGGKQ 60
 Db 1 MALMRSSDNLVYLPPEPSVAVLSDVDYVYTNITNYAGSTRLLTVGHPYPIRKSSNKA 60
 QY 61 DIPKVSAYQYRVRVOLPDNPKFGLPDNSLYNPTQRLVWACAGVEIGRCQYGLVGS 120
 Db 61 DVPEKVSAYQYRVRVRVLPDNNKFGLPDARLYNDAERLVWACAGVEIGRCQYGLVGS 120
 QY 121 PFYKLLDDESSHAATSNVSEEDYVDNYSVYKOTQCTICGAPALGHNKAGKRSRL 180
 Db 121 PLTKLLDDESSHAATSNVSEEDYVDNYSVYKOTQCTICGAPALGHNKAGKRSRL 179
 QY 181 SGGDCPELEKNTVLEDGMDVDTGYGAMDESTLDPTKCEVPLDICSICKPYDYLQMSAD 240
 Db 180 SGGDCPELEITAPIDGMDVDTGYGAMDEGNLSNKSVDPLDICTCKKPYDYLQMAAE 239
 QY 241 PYGDSMEFCLRRQDLFARHFWNRAGTMDVPOSlyTKGTM-RASFGSCVYSPSPSG 299
 Db 240 PYGDSMEFCLRRQDLFARHFWNRAGTMDVPOSlyTKGTM-RASFGSCVYSPSPSG 299
 QY 300 VTSDSOLEFNKPYWLHKAQGNHNGICWNOLEFVTVDTSTNTLTICASTQSPVPGQYD 359
 Db 300 ISSBAOLEFNKPYWLHKAQGNHNGICWNOLEFVTVDTSTNTLTICASTQSPVPGQYD 357
 QY 360 KFKQYSRVEEDLQFIQOLCTITLTADVASTIHSNSSLIEDMNFVPPPTSLVDY 419
 Db 358 KFKEXLRGEEYDQFIQOLCKVTLTPEIMAYLHTMNSTLLEDNMFGLTLPSTSLIED 417
 QY 420 RFVQSVAITCOKDAPPAENKDPYDKLFKFWNVDLKKEFSLLDQYLRGRFLVQAQLRR 479
 Db 418 RFISSSAITCOKDAPPTKEDPYAKLNFMDVDLKRFSLDLSQFPLGRKFLMQLGVARS 477
 QY 480 TIGPKRSAPSATYSSSKPAKRVYR 504
 Db 478 SVSVYKRPA-STTRGSSAAKRRKRAK 501

RESULT 10

VL1_HPV10 STANDARD; PRF: 531 AA.

ID VL1_HPV10

AC P36732;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Major capsid protein L1.

GN L1.

OS Human papillomavirus type 10.

OC Viruses; dsDNA viruses, no RNA stage: Papillomaviridae;

OC Papillomavirus.

OX NCBI_Taxid=10603;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94265501; Pubmed=8205838;

RA Delius H., Hofmann B.;

RT "Primer-directed sequencing of human papillomavirus types."

RT Curr. Top. Microbiol. Immunol. 186:13-31(1994).

CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-29 IS THE INITIATOR.

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CC -----

CC EMBL: X74465; CA52494.1; -

DR PIR: S36537; S36537.

DR InterPro: IPR002210; PV_capsid.L1.

DR Pfam: PF00500; late_protein.L1; 1.

DR PRINTS: PR00865; HPVcapsid.L1.

DR ProdDom: PD000544; PV_capsid.L1; 1.
 KW Coat protein; Late protein.
 SQ SEQUENCE 531 AA; 59011 MW; EDC9BA0DCA7A67F6 CRC64;

Query Match 69.8%; Score 1909; DB 1; Length 531;
 Best Local Similarity 67.9%; Pred. No. 9.2e-158;
 Matches 342; Conservativity 70; Mismatches 90; Indels 2; Gaps 2;

QY 1 MALMRSDMTVYLPPPSVARVNTDDYVTRTSIFYHAGSSRLTLVGNPFYRVAGGNKQ 60
 DB 29 MALMRSSDNLVYLPFPVSKVLTSDDYVTRTNIYYAGSRLLTVGHPEFIPKSSNNKY 88
 QY 61 DIPKVSAYQYRVFVQLPDPNKGFLPDNSIYNPETORLWACAGVEIGRQPLGVLSGH 120
 DB 89 DVPKVSAYQYRVFVRLPDPNKGFLPDNARLYNDARLWACAGVEIGRQPLGVLSGH 148
 QY 121 PFYKRLDDESSHAATSNVSEEDVADNVSDYKOTQCLIGCAPAIGEHNAKGTACKSRPL 180
 DB 149 PLTKNLEDEENSIAGPIGQDSRDNIYDNKOTQCLIGCTPPGEHMGKGTPCRNP 207
 QY 181 SOGDCPPELEKNTVLEDDGMVDTGYGAMDFSLQDKCEVPLDQCOSICKYPPYLQMSAD 240
 DB 208 AOGDCPPELEKNTSPIDGDMVDTGYGAMDFSLQDKCEVPLDQCOSICKYPPYLQMAAE 267
 QY 241 PYGDSMEFCLRRQQLFARHFNAGTMGDTVPQSLYIKGTGMRAFGSCVYSPSGSIY 300
 DB 268 DVPKVSAYQYRVFVRLPDPNKGFLPDNARLYNDARLWACAGVEIGRQPLGVLSGH 327
 QY 301 TSDSQLEFNKPYMLHKAQGNHNGICWGNOLFYVYVDTTRSTNLTCASTOSPPVGOYDATK 360
 DB 328 TSEAQLFENKPYMLHKAQGNHNGICWGNOLFYVYVDTTRSTNLTCASTOSPPVGOYDATK 387
 QY 361 FKQYSHVEEYDLOFLOCTITLADVNSYIHSNSSLIEDMNFVPPPTSLVDYR 420
 DB 388 FKEXYLRHGEYDLOFLOCTITLADVNSYIHSNSSLIEDMNFVPPPTSLVDYR 447
 QY 421 FVQSVATITCOKDAAPAKENDPYDKLKFVNVDLKEKESLDLDQYPLGRKFLVQGLRRKPT 480
 DB 448 FVSSSLATITCOKDPPAKEDPYDLAKYFVNVDLKDRFSLDQPLGRKFLVQGLRRKPT 507
 QY 481 IGPKRSAPSATTSSSKPAKRVYR 504
 DB 508 VSVRRKRPATSA-TGSAFAKRRKTK 530

RESULT 11
 ID VIL_HPV30 STANDARD; PRT; 508 AA.
 AC 002515;

DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Major capsid protein L1.
 GN L1.
 OS Human papillomavirus type 30.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_Taxid=10611;
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE=94265501; PubMed=8205838;
 RA Dellus H., Hofmann B.;
 RT "Primer-directed sequencing of human papillomavirus types.";
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
 RP SEQUENCE OF 309-352 FROM N.A.
 RX MEDLINE=92407963; PubMed=13326639;
 RA Chan S.Y., Bernard H.U., Ong C.K., Chan S.P., Birgit H., Dellus H.;
 RT "Phylogenetic analysis of 48 papillomavirus types and 28 subtypes and
 variants: a showcase for the molecular evolution of DNA viruses.";
 RL J. Virol. 66:5714-5725(1992).

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DR EMBL: X74474; CAA52548.1; -;
 DR EMBL: M96279; AAA47018.1; -;
 DR PIR: S36508; S36508.
 DR InterPro: IPR002210; PV_capsid.L1.
 DR Pfam: PF00500; Late_protein.L1.
 DR PRINTS: PR00865; HPVcapsid.L1.
 DR ProdDom: PD000544; PV_capsid.L1; 1.
 KW Coat protein; Late protein.
 SQ SEQUENCE 508 AA; 56667 MW; 62F359F257714748 CRC64;

Query Match 68.8%; Score 1879; DB 1; Length 508;
 Best Local Similarity 67.1%; Pred. No. 3.5e-155;
 Matches 337; Conservativity 82; Mismatches 81; Indels 2; Gaps 1;

QY 1 MALMRSDMTVYLPPPSVARVNTDDYVTRTSIFYHAGSSRLTLVGNPFYRVAGGNKQ 60
 DB 8 MALMRSEKTVYLPFPVSKVLTSDDYVTRTNIYYAGSRLLTVGHPEFIPKSSNNKY 67
 QY 61 DIPKVSAYQYRVFVQLPDPNKGFLPDNSIYNPETORLWACAGVEIGRQPLGVLSGH 120
 DB 68 DVPKVSAYQYRVFVRLPDPNKGFLPDNARLYNDARLWACAGVEIGRQPLGVLSGH 127
 QY 121 PFYKRLDDESSHAATSNVSEEDVADNVSDYKOTQCLIGCAPAIGEHNAKGTACKSRPL 180
 DB 128 PFENKLDDESSSTIANQDTAEDSRDNIYDNKOTQCLIGCTPPGEHMGKGTPCRNP 187
 QY 181 SOGDCPPELEKNTVLEDDGMVDTGYGAMDFSLQDKCEVPLDQCOSICKYPPYLQMSAD 240
 DB 188 AOGDCPPELEKNTSPIDGDMVDTGYGAMDFSLQDKCEVPLDQCOSICKYPPYLQMAAE 247
 QY 241 PYGDSMEFCLRRQQLFARHFNAGTMGDTVPQSLYIKGTGMRAFGSCVYSPSGSIY 300
 DB 248 AYGDSMWFYLRBQQLFARHFNAGTMGDTVPQSLYIKGTGMRAFGSCVYSPSGSIY 307
 QY 301 TSDSQLEFNKPYMLHKAQGNHNGICWGNOLFYVYVDTTRSTNLTCASTOSPPVGOYDATK 360
 DB 308 TSEAQLFENKPYMLHKAQGNHNGICWGNOLFYVYVDTTRSTNLTCASTOSPPVGOYDATK 365
 QY 361 FKQYSHVEEYDLOFLOCTITLADVNSYIHSNSSLIEDMNFVPPPTSLVDYR 420
 DB 366 IKQYSHVEEYDLOFLOCTITLADVNSYIHSNSSLIEDMNFVPPPTSLVDYR 425
 QY 421 FVQSVATITCOKDAAPAKENDPYDKLKFVNVDLKEKESLDLDQYPLGRKFLVQGLRRKPT 480
 DB 426 YKSLATITCOKDPPAKEDPYDLAKYFVNVDLKDRFSLDQPLGRKFLVQGLRRKPT 485
 QY 481 IGPKRSAPSATTSSSKPAKRVYR 502
 DB 486 TTKKRSAPSSSTSPSAKRRK 507

RESULT 12
 ID VIL_HPV26 STANDARD; PRT; 503 AA.
 AC P36735;

DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Major capsid protein L1.
 GN L1.
 OS Human papillomavirus type 26.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_Taxid=31549;
 RN RP SEQUENCE FROM N.A.

RX MEDLINE=94265501; PubMed=6205638;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
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CC -----
DR EMBL; X74472; S36549.1; -
DR PIR; S36549; S36549.
DR InterPro; IPR002210; PY_capsid.L1.
DR Pfam; PF00500; late.protein.L1; 1.
DR PRINTS; PR00865; HPCAPSIDL1.
DR ProDom; PD000544; PY_capsid.L1; 1.
DR Coat protein; Late protein.
SQ SEQUENCE 503 AA; 56328 MW; A0706D12P425BE80 CRC64;

Query Match 68.1%; Score 1861.5; DB 1; Length 503;
Best Local Similarity 67.3%; Pred. No. 1.le-153;
Matches 337; Conservative 70; Mismatches 91; Indels 3; Gaps 3;

QY 1 MALMRPSDNVYLLPPPPVARYVNTDVTYRTSIFYHAGSSRLTLVGNPFYRVPAAGGNKQ 60
DB 1 MALMRPSDNVYLLPPPPVARYVNTDVTYRTSIFYHAGSSRLTLVGNPFYRVPAAGGNKQ 59
QY 61 DIPVSAQYRVFRVQLPDPNKGFLPDNSIYNPEFQRLYMACAGVEIGRGPVLGVLGGH 120
DB 60 EIPVSAQYRVFRVQLPDPNKGFLPDNSIYNPEFQRLYMACAGVEIGRGPVLGVLGGH 119
QY 121 PFYNNKLDTESSHAATSNVEDVNDVSVYKQOTOLCILGAPAIGEHMAKGTACKSRPL 180
DB 120 PLFKKLDTESSHAATSNVEDVNDVSVYKQOTOLCILGAPAIGEHMAKGTACKSRPL 179
QY 181 SQGDCCPLELKNVLEDDGMDVDTGYGAMDEFTLQDTCKEVPDLQCSICKYPDYLYQMSAD 240
DB 180 SQGDCCPLELKNVLEDDGMDVDTGYGAMDEFTLQDTCKEVPDLQCSICKYPDYLYQMSAD 239
QY 241 PYGDSMFCFLREQLFARHFNWAGTMDVTPQSLYIKGT-GMARSPPSCYVSSPSGSI 299
DB 240 PYGDSMFCFLREQLFARHFNWAGTMDVTPQSLYIKGT-GMARSPPSCYVSSPSGSI 299
QY 300 VTSQSOLFENKPYWLHKAQGHNNGICWNQLFVTVDFTSTNLITCASTQSPVPGQYDAT 359
DB 300 VTSQSOLFENKPYWLHKAQGHNNGICWNQLFVTVDFTSTNLITCASTQSPVPGQYDAT 359
QY 360 KFKQYSRHVEYDIQIFQCTITLADVMSYIHSNNSILEDNMFVGPPTSLVDYTY 419
DB 360 KFKQYSRHVEYDIQIFQCTITLADVMSYIHSNNSILEDNMFVGPPTSLVDYTY 419
QY 420 RFVQSVATTCOKDAPAKNKDPYDKIKFWNDLKEKESLDDQYPLGKFLVQAGLRPK 479
DB 420 RFVQSVATTCOKDAPAKNKDPYDKIKFWNDLKEKESLDDQYPLGKFLVQAGLRPK 479
QY 480 TIGPKRSAPSATTSKPKAKR 500
DB 480 TIGPKRSAPSATTSKPKAKR 499
QY 480 KLG-TKRLPSSSTSSSTKRRK 499
DB 480 KLG-TKRLPSSSTSSSTKRRK 499

RESULT 13
VL1 HPV61
ID VL1 HPV61 STANDARD; PRT; 505 AA.
AC P50822; 080954;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Major capsid protein L1.
GN L1
OS Human papillomavirus type 61.

CC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
NCBI_TaxID=37116;
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 317-468 FROM N.A.
RX MEDLINE=95052821; PubMed=7963696;
RA Bernard H.U., Chan S.Y., Manos M.M., Ong C.K., Villa L.L.,
RT "Identification and assessment of known and novel human
RT papillomaviruses by polymerase chain reaction amplification,
RT restriction fragment length polymorphisms, nucleotide sequence, and
RT phylogenetic algorithms";
RL J. Infect. Dis. 170:1077-1085(1994).
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CC -----
DR EMBL; U31793; AAA79498.1; -
DR EMBL; U12500; AAA67244.1; -
DR InterPro; IPR002210; PY_capsid.L1.
DR Pfam; PF00500; late.protein.L1; 1.
DR PRINTS; PR00865; HPCAPSIDL1.
DR ProDom; PD000544; PY_capsid.L1; 1.
DR Coat protein; Late protein.
FT CONFLICT 374 374 Q -> P (IN REF. 2).
FT CONFLICT 430 430 Q -> L (IN REF. 2).
SQ SEQUENCE 505 AA; 56710 MW; EB56C4A60E94C853 CRC64;

Query Match 67.9%; Score 1855.5; DB 1; Length 505;
Best Local Similarity 66.5%; Pred. No. 3.8e-153;
Matches 337; Conservative 69; Mismatches 94; Indels 7; Gaps 5;

QY 1 MALMRPSDNVYLLPPPPVARYVNTDVTYRTSIFYHAGSSRLTLVGNPFYRVPAAG--GN 58
DB 1 MALMRPSDNVYLLPPPPVARYVNTDVTYRTSIFYHAGSSRLTLVGNPFYRVPAAG--GN 60
QY 59 KODIPKVSAYQYRVFRVQLPDPNKGFLPDNSIYNPEFQRLYMACAGVEIGRGPVLGVLGGH 118
DB 61 KNTIPKVSAYQYRVFRVQLPDPNKGFLPDNSIYNPEFQRLYMACAGVEIGRGPVLGVLGGH 120
QY 119 GHPPYNNKLDTESSHAATSNVEDVNDVSVYKQOTOLCILGAPAIGEHMAKGTACKSR 178
DB 121 GHPPYNNKLDTESSHAATSNVEDVNDVSVYKQOTOLCILGAPAIGEHMAKGTACKSR 179
QY 179 PLGSGCCPLELKNVLEDDGMDVDTGYGAMDEFTLQDTCKEVPDLQCSICKYPDYLYQMS 238
DB 180 PLGSGCCPLELKNVLEDDGMDVDTGYGAMDEFTLQDTCKEVPDLQCSICKYPDYLYQMS 239
QY 180 APRPTDCEPLEFTYTTIQQDGMVETGIGALDFALQENKKEVPLDITCTTCKIPDYLYQMA 239
DB 239 ADPYGDSMFCFLREQLFARHFNWAGTMDVTPQSLYIKGT-GMARSPPSCYVSSPSGSI 298
QY 240 AEPLYGDSMFCFLREQLFARHFNWAGTMDVTPQSLYIKGT-GMARSPPSCYVSSPSGSI 299
DB 300 MVSSDSOLFENKPYWLHKAQGHNNGICWNQLFVTVDFTSTNLITCASTQSPVPGQYDA 358
QY 359 TVTSQSOLFENKPYWLHKAQGHNNGICWNQLFVTVDFTSTNLITCASTQSPVPGQYDA 358
DB 359 TKFKQYSRHVEYDIQIFQCTITLADVMSYIHSNNSILEDNMFVGPPTSLVDYTY 418
QY 419 YRFQSVATTCOKDAPAKNKDPYDKIKFWNDLKEKESLDDQYPLGKFLVQAGLR 477
DB 419 YRFQSVATTCOKDAPAKNKDPYDKIKFWNDLKEKESLDDQYPLGKFLVQAGLR 478

QY 478 KPTIGPKRSAPSATTSSKPAKRRVYR 504
 DB 479 VSV--SRKRAAPSSTPTSSPATKRRKR 503

RESULT 14

V1L_HPV53 STANDARD: PRT: 499 AA.

AC 005113;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Major capsid protein L1.

GN L1.

OS Human papillomavirus type 53.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.

OX NCBI_TaxID=10619;

RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=94265501; PubMed=8205838;
 RA Delius H., Hofmann B.;

RT "Primer-directed sequencing of human papillomavirus types.";
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).

RN [2]

RP SEQUENCE OF 300-343 FROM N.A.
 RX MEDLINE=92407963; PubMed=1326639;

RA Chan S.Y., Bernard H.U., Ong C.K., Chan S.P., Birgit H., Delius H.;
 RT "Phylogenetic analysis of 48 papillomavirus types and 28 subtypes and
 variants: a showcase for the molecular evolution of DNA viruses.";

RL J. Virol. 66:5714-5725(1992).

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CC EMBL: X74482; CAA52595.1; -

DR EMBL: M96298; AAA47037.1; -

DR PIR: S36531; S36531.

DR InterPro: IPR002210; PV_capsid_L1.

DR Pfam: PF00500; Late-Protein_L1; 1.

DR PRINTS: PR00865; HPVcapsid.L1.

DR ProDom: PD000544; PV_capsid_L1; 1.

DR Coat protein; Late protein.

SQ SEQUENCE 499 AA; 55722 MW; 5221961A3FDD5A66 CRC64;

Query Match 67.9%; Score 1855; DB 1; Length 499;
 Best local Similarity 66.3%; Pred. No. 4.1e-153;

Matches 333; Conservative 78; Mismatches 87; Indels 4; Gaps 2;

QY 1 MALMRPSDNTVYLPPPSVARYVNTDYVTRTSIFHAGSSRLITVGNPFYRPVAGGNQ 60

DB 1 MAWMRPSDSKVTLPPVPSKVITTDAYVKTIFHAGSSRLITVGHPRYPPIPSKSG--KA 58

QY 61 DIPKVSAYQYRVRYQLPDPNKFGLPDNSIYPERQRLVWACAGVEIGGQPLGVLSGH 120

DB 59 DIPKVSAGFYRVRYRLPDPNKFGLPDNTIFNPDGERLVWACVGLGIGQPLGVVSSH 118

QY 121 PPNKLDITDESSHAATSNVSEVDVNDVYKOTQICIGCAPAIGEHNAKGTACKSRPL 180

DB 119 PPNKLDITDESSSIADTPADPSRDVSVDPKOTQICIGCAPAIGEHNTKGTACKSRPT 178

QY 181 SGGDCPPELTKNTVLEDDGMVDTGAMDFSTLQDTKCEVPLDIOQSTICKYDYLQMSAD 240

DB 179 TGGDCPPELTLNPSLEDGMVDTGFGALNFKALQESKSDVPLDIVQSTCKYDYLKMSAD 238

QY 241 PYGDSMFCLRRQQLFARHFNRRAGTMDTVPQSLYIKGTGMRASGSCVYSPSPSGSIV 300

DB 239 AVGDSMWFYLRREQQLFTRHFNRRAGTMDTVPQSLYIKGTGMRASGSCVYSPSPSGSIV 298

QY 301 TSDSQLEPNKPYWLHKAQGHNNIGICWHNQLFVTVVDTTSTNTLTICASTQSPVPGQDARK 360
 DB 299 TSEAQLFNKPYWLQRAQGHNNIGICWHNQLFVTVVDTTSTNTLTICASTQSPVPGQDARK 356
 QY 361 FKOYSRHVEYDQLEFQICITITLADWMSYHSNMSSTLEDMNFEVPPPTSLVDTR 420
 DB 357 IKOYVRHAEVEYDQLEFQICITITLADWMSYHSNMSSTLEDMNFEVPPPTSLVDTR 416
 QY 421 FVQSVATITCQKADAPAPENKDPYDKLKFWMVNDLKEKESLIDQYPLGRKFLVQAGRRKPT 480
 DB 417 YVSAATITCQKADAPAPENKDPYDKLKFWMVNDLKEKESLIDQYPLGRKFLVQAGRRKPT 476
 QY 481 IGPKRRSAPSATTSSKPAKRRVYR 502
 DB 477 VSSKRRSASTTSPADSRRKR 498

RESULT 15

V1L_RHPV1 STANDARD: PRT: 501 AA.

AC P22163;
 DT 01-FEB-1991 (Rel. 19, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Major capsid protein L1.

GN L1.

OS Rhesus papillomavirus type 1 (Rhpv 1).
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.

OX NCBI_TaxID=10570;

RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=91135018; PubMed=1847267;

RA Ostrow R.S., Labresh K.V., Fairs A.J.;

RT "Characterization of the complete Rhpv 1 genomic sequence and an

RT integration locus from a metastatic tumor.";

RL Virology 181:424-429(1991).

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CC EMBL: M60184; AAA79318.1; -

DR PIR: H38503; P1WKR1.

DR InterPro: IPR002210; PV_capsid_L1.

DR Pfam: PF00500; Late-Protein_L1; 1.

DR PRINTS: PR00865; HPVcapsid.L1.

DR ProDom: PD000544; PV_capsid_L1; 1.

DR Coat protein; Late protein.

SQ SEQUENCE 501 AA; 55635 MW; 6E808DBF130E440A CRC64;

Query Match 67.9%; Score 1855; DB 1; Length 501;
 Best local Similarity 67.1%; Pred. No. 4.1e-153;

Matches 338; Conservative 66; Mismatches 96; Indels 4; Gaps 3;

QY 1 MALMRPSDNTVYLPPPSVARYVNTDYVTRTSIFHAGSSRLITVGNPFYRPVAGGNQ 60

DB 1 MSWMRPSDSKVTLPPVPSKVITTDAYVKTIFHAGSSRLITVGHPRYPPIPSKSG--GNKV 59

QY 61 DIPKVSAYQYRVRYQLPDPNKFGLPDNSIYPERQRLVWACAGVEIGGQPLGVLSGH 120

DB 60 SVPKVSGLODYRVRYRLPDPNKFGLPDANFYDPNQLVWACVGLGIGQPLGVLSGH 119

QY 121 PPNKLDITDESSHAATSNVSEVDVNDVYKOTQICIGCAPAIGEHNAKGTACKSRPL 180

DB 120 PLNKLKDTDENGPKVAGGAGANNRECVSDYKOTQICIGCAPAIGEHNAKGTACKSRPL 177

QY 181 SGGDCPPELTKNTVLEDDGMVDTGAMDFSTLQDTKCEVPLDIOQSTICKYDYLQMSAD 240

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OM protein - protein search, using sw model

Run on: October 17, 2003, 10:55:25 ; Search time 68.0888 Seconds
(without alignments)
1921.499 Million cell updates/sec

Title: US-08-913-644-2

Perfect score: 2733
Sequence: 1 MALMRPSDNTVYLPPPSVAR.....APSATTSSKPAKRVRRANK 507

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database .:

1: SP:REMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phase:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertibrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2457.5	89.9	536	4	O9Y4Y5	O9Y4Y5 homo sapien
2	2223.5	81.4	504	12	O9WHG7	O9WHG7 human papill
3	2223.5	81.4	508	12	O81971	O81971 human papill
4	1954	71.5	565	12	O86951	O86951 human papill
5	1917.5	70.2	504	12	O81961	O81961 human papill
6	1909	69.8	503	12	O81958	O81958 human papill
7	1870	68.4	518	12	O81958	O81958 human papill
8	1862.5	68.1	525	12	O8B5X1	O8B5X1 human papill
9	1861	68.1	503	12	O99323	O99323 human papill
10	1852	67.8	503	12	O91R52	O91R52 human papill
11	1836	67.2	503	12	O99FW7	O99FW7 human papill
12	1830.5	67.0	504	12	O81017	O81017 human papill
13	1828	66.9	505	12	O9W4G5	O9W4G5 human papill
14	1828	66.9	505	12	O81015	O81015 human papill
15	1828	66.9	531	12	O8B5N5	O8B5N5 human papill
16	1827.5	66.9	506	12	O82004	O82004 human papill

17	1827.5	66.9	534	12	O82003	O82003 human papill
18	1826	66.8	505	12	O9W4G6	O9W4G6 human papill
19	1826	66.8	505	12	O9WHS6	O9WHS6 human papill
20	1826	66.8	505	12	O9WHS5	O9WHS5 human papill
21	1826	66.8	531	12	O00530	O00530 human papill
22	1822	66.7	505	12	O92282	O92282 human papill
23	1822	66.7	531	12	O8B5N9	O8B5N9 human papill
24	1821	66.6	505	12	O9WHS7	O9WHS7 human papill
25	1819	66.6	505	12	O9WPH4	O9WPH4 human papill
26	1807	66.1	507	12	O9JH44	O9JH44 human papill
27	1803	66.0	494	12	O80999	O80999 human papill
28	1802	65.9	494	12	O81011	O81011 human papill
29	1802	65.9	494	12	O81004	O81004 human papill
30	1802	65.9	494	12	O80996	O80996 human papill
31	1802	65.9	494	12	O80997	O80997 human papill
32	1802	65.9	494	12	O81000	O81000 human papill
33	1801	65.9	494	12	O81005	O81005 human papill
34	1801	65.9	494	12	O81007	O81007 human papill
35	1799	65.8	494	12	O81002	O81002 human papill
36	1799	65.8	505	12	O91AX0	O91AX0 human papill
37	1798.5	65.8	565	12	O9BHD3	O9BHD3 human papill
38	1798	65.8	494	12	O81003	O81003 human papill
39	1797	65.8	494	12	O80998	O80998 human papill
40	1797	65.8	503	12	O9WNA4	O9WNA4 human papill
41	1796	65.7	494	12	O81008	O81008 human papill
42	1796	65.7	494	12	O90204	O90204 human papill
43	1794	65.6	494	12	O81006	O81006 human papill
44	1792	65.6	494	12	O81010	O81010 human papill
45	1792	65.6	494	12	O81009	O81009 human papill

ALIGNMENTS

RESULT 1

ID	O9Y4Y5	PRELIMINARY;	PRT;	536 AA.
AC	O9Y4Y5;			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	L1 protein.			
GN	HPV45 L1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Sastre-Garau X., Favre M., Couturier J., Orth G.;			
RT	"Distinct patterns of alteration of myc genes associated with			
RT	integration of human papillomavirus type 16 oe type 45 in two genital			
RT	tumours."			
RL	J. Gen. Virol. 81:198-199(2000).			
DR	EMBL; AJ242956; CAB44705.1; -			
DR	InterPro; IPR002210; PV_capsid_L1.			
DR	Pfam; PF00500; late_protein_L1; 1.			
DR	PRINTS; PR00865; HPVcapsidL1.			
DR	ProDom; PD000544; PV_capsid_L1; 1.			
DR	SEQUENCE 536 AA; 60075 MW; 90498497AA4C807 CRC64;			
QY	Query Match	89.9%;	Score 2457.5;	DB 4; Length 536;
QY	Best Local Similarity	87.6%;	Pred. No. 1.9e-212;	
QY	Matches 44;	Conservative 29;	Mismatches 31;	Indels 3; Gaps 2;

QY	1	MALMRPSDNTVYLPPPSVARVNTDYYRTSTIFYAGSSRLTVCNPFYR-VPAGGKMK 59
DB	27	MALMRPSDNTVYLPPPSVARVNTDYYRTSTIFYAGSSRLTVCNPFYRVPAGGKMK 86
QY	60	QDPKVSAYQYRFRQLPDPNKEG.PDINSIVNPEIORLVMACAGVEIRGQPLGVGLSG 119
DB	87	QAVPKVSAYQYRFRQLPDPNKEG.PDINSIVNPEIORLVMACAGVEIRGQPLGVGLSG 146

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QY 120 HPEYKLLDTESSHAATSNVEDYDNDVYKOTQOLCIGCAPAIGEHMAKGTACKSRP 179
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 147 HPEYKLLDTESSHAATAAIAVITQVDNDVYKOTQOLCIGCAPAIGEHMAKGTACKRPAQ 206
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 LSQDCCPLELKNVTLEGGDMVDYGYGAMDSSTLODRCEVPLDICOSICKYPPYLOMSA 239
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 207 LQPDCCPLELKNVTLEGGDMVDYGYGAMDSSTLODRCEVPLDICOSICKYPPYLOMSA 266
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 DPYDSMFECLRRQELFARHFWNAGTMGDVYPOSLYIKGT--GMRASPGSCVSPSPSG 297
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 267 DPYDSMFECLRRQELFARHFWNAGTMGDVYPOSLYIKGT--GMRASPGSCVSPSPSG 326
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 298 STYVSQLEFNKPYWLAKAGHNNICWNQLEFVYVDTTRSTNLTICASTQSPYQGYD 357
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 327 STYVSQLEFNKPYWLAKAGHNNICWNQLEFVYVDTTRSTNLTICASTQSPYQGYD 386
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 358 ATKFOYSRHYEEDLOFIFOLCTITTLADVNSYIHSNSSLIEDMNGVPPPTSLYD 417
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 387 PTRKXHSRHYEEDLOFIFOLCTITTLADVNSYIHSNSSLIEDMNGVPPPTSLYD 446
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 418 TYRFVQSAVITQKDAAPAEKNKDPYDKLKFVNVDLKEKFSLLDQYPLGRKFLVQAGLR 477
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 447 TYRFVQSAVITQKDAAPAEKNKDPYDKLKFVNVDLKEKFSLLDQYPLGRKFLVQAGLR 506
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 478 KPTIGPKRRSAPATSSSKPAKRVYRARK 507
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 507 KPTIGPKRRSAPATSSSKPAKRVYRARK 536
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 2

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Q9WHG7 PRELIMINARY: PRT: 504 AA.
ID Q9WHG7
AC Q9WHG7;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DR 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Putative major capsid protein L1.
CN L1.
OS Human papillomavirus candidhpv65.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=151757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20047972; PubMed=10580054;
RA Chow V.T.K., Leong P.W.F.;
RT "Complete nucleotide sequence, genomic organization and phylogenetic
analysis of a novel genital human papillomavirus type, HLT7474-S."
RL J. Gen. Virol. 80:2923-2929 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Chow V.T.K., Leong W.F.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131950; AAD24188.1;
DR InterPro; IPR002210; PV_capsid.L1.
DR Pfam; PF00500; late_protein.L1; 1.
DR PRINTS; PR00865; HPVcapsid.L1.
DR PRODOM; PD000544; PV_capsid.L1; 1.
SQ SEQUENCE 504 AA; 56435 MW; 3852CE9203E3D839 CRC64;

```

Query Match 81.4%; Score 2223.5; DB 12; Length 504;
 Best Local Similarity 79.7%; Pred. No. 2e-191;
 Matches 400; Conservative 47; Mismatches 54; Indels 1; Gaps 1;

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QY 1 MALMRPSDNTVYLPPEPSAVRVNTDDVYTRTSIFYHAGSSRLTLVGNPYFVPAGGNGKQ 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MALMRSSDSKYLPPEPSAVRVNTDDVYTRTSIFYHAGSSRLTLVGNPYFVPAGGNGKQ 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DIPKVSAYQYRVEFVQLPDPNKFGLPDNSTIYNPETQRLVMACAGVEIGRQPLGVLSGH 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DIPKVSAYQYRVEFVQLPDPNKFGLPDNSTIYNPETQRLVMACAGVEIGRQPLGVLSGH 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 PFYKLLDTESSHAATSNVEDYDNDVYKOTQOLCIGCAPAIGEHMAKGTACKSRPL 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 121 PFYKLLDTESSHAATSNVEDYDNDVYKOTQOLCIGCAPAIGEHMAKGTACKRGAV 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 SOGDCPPLELKNVTLEGGDMVDYGYGAMDSSTLODRCEVPLDICOSICKYPPYLOMSAD 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 QTGDCPPLELKNVTLEGGDMVDYGYGAMDSSTLODRCEVPLDICOSICKYPPYLOMSAD 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 PYGDSMFECLRRQELFARHFWNAGTMGDVYPOSLYIKGTGMRASPGSCVSPSPSGIV 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 AYGDSMFECLRRQELFARHFWNAGTMGDVYPOSLYIKGTGMRASPGSCVSPSPSGIV 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 TSDSQLEFNKPYWLAKAGHNNICWNQLEFVYVDTTRSTNLTICASTQSPYQGYD 360
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 SSDAQNENKPYWLAKAGHNNICWNQLEFVYVDTTRSTNLTICASTQSPYQGYD 360
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 FKOYSRHYEEDLOFIFOLCTITTLADVNSYIHSNSSLIEDMNGVPPPTSLYD 420
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 FKETRYRHYEEDLOFIFOLCTITTLADVNSYIHSNSSLIEDMNGVPPPTSLYD 420
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 FVQSAVITQKDAAPAEKNKDPYDKLKFVNVDLKEKFSLLDQYPLGRKFLVQAGLRKPT 480
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 FVQSAVITQKDAAPAEKNKDPYDKLKFVNVDLKEKFSLLDQYPLGRKFLVQAGLRKPT 480
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 IGPKRRSAPATSSSKPAKRVYRARK 502
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 IGPKRRSAPATSSSKPAKRVYRARK 501
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 3

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Q81971 PRELIMINARY: PRT: 508 AA.
ID Q81971
AC Q81971;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DR 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ORF putative L1 protein.
CN L1.
OS Human papillomavirus type 59.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=37115;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94303229; PubMed=8030272;
RA Kuo J., Roy-Burman A., Kim H., de Villiers E.M., Matsukura T.,
RT "Nucleotide sequence and phylogenetic classification of human
papillomavirus type 59."
RL Virology 203:158-161 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Choe J.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; X77858; CA54856.1;
DR InterPro; IPR002210; PV_capsid.L1.
DR Pfam; PF00500; late_protein.L1; 1.
DR PRINTS; PR00865; HPVcapsid.L1.
DR PRODOM; PD000544; PV_capsid.L1; 1.
SQ SEQUENCE 508 AA; 56841 MW; FB9A2D8C009EA5BA CRC64;

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Query Match 81.4%; Score 2223.5; DB 12; Length 508;
 Best Local Similarity 79.4%; Pred. No. 2e-191;
 Matches 400; Conservative 49; Mismatches 54; Indels 1; Gaps 1;

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QY 1 MALMRPSDNTVYLPPEPSAVRVNTDDVYTRTSIFYHAGSSRLTLVGNPYFVPAGGNGKQ 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MALMRSSDSKYLPPEPSAVRVNTDDVYTRTSIFYHAGSSRLTLVGNPYFVPAGGNGKQ 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DIPKVSAYQYRVEFVQLPDPNKFGLPDNSTIYNPETQRLVMACAGVEIGRQPLGVLSGH 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DIPKVSAYQYRVEFVQLPDPNKFGLPDNSTIYNPETQRLVMACAGVEIGRQPLGVLSGH 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 PFYKLLDTESSHAATSNVEDYDNDVYKOTQOLCIGCAPAIGEHMAKGTACKSRPL 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 121 PLYNKLDITENSHVSAVDTKTRDNVSVDYKOTOLCTICGCPAIGEHNTKCTACKPTTV 180
QY 181 SOGDCPPELEKNTVLEEDGMDVDTGYGAMDFSTLQDTCBEPVLDICQSTICKYEDYLOMSAD 240
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 181 VQGDPEPLELINTPIEDGMDVDTGYGAMDFKLLQDNKSEVPDLICQSTICKYEDYLOMSAD 240
QY 241 PYGDSMFELRREQLFARHFNRAGTGTVPQSLYIKTKGMRASGSCVYSPSGSIV 300
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 241 AGDSMFELRREQLFARHFNRAGTGTVPQSLYIKTKGMRASGSCVYSPSGSIV 300
QY 301 TSDSOLFENKPYLHKAQGNNGICWNNOLFTVVTTRSTNTLTICASTOSPPVGOYDATK 360
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 301 TSDSOLFENKPYLHKAQGNNGICWNNOLFTVVTTRSTNTLTICASTOSPPVGOYDATK 360
QY 361 FKQYSHVEEYDLOFTFOLCTITLTADVNSYIHSNNSILEDWNFVPPPTSLVDYTR 420
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 361 FKQYSHVEEYDLOFTFOLCTITLTADVNSYIHSNNSILEDWNFVPPPTSLVDYTR 420
QY 421 FVQSAVITCQKXVAPTEKQDPYAKLNFVMDLKDREITLDSQPLGRKFLDIGNARRSV 542
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 421 FVQSAVITCQKXVAPTEKQDPYAKLNFVMDLKDREITLDSQPLGRKFLDIGNARRSV 542
QY 481 IGPKRKRSAPSATSSKPAKRVRR 504
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 481 IGPKRKRSAPSATSSKPAKRVRR 504
QY 481 IGPKRKRSAPSATSSKPAKRVRR 504
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 481 IGPKRKRSAPSATSSKPAKRVRR 504
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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RESULT 4
056951 PRELIMINARY: PRT: 565 AA.
AC 056951:
ID 056951:
AC 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE L1 protein.
GN L1.
OS Human papillomavirus type 77.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=69986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98118461; PubMed=9454709;
RA Delius H., Saegling B., Bergmann K., Shamanin V., de Villiers E.M.;
RT "The genomes of three of four novel HPV types, defined by differences
RT of their L1 genes, show high conservation of the E7 gene and the
RT URR.";
RL Virology 240:359-365(1998).
DR EMBL: Y15175; CAA75468.1;
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1.
DR PRINTS: PR00865; HPVcapsidL1.
DR ProDom: PD000544; PV_capsid_L1.
SQ SEQUENCE 565 AA; 63377 MW; 393B5933F9480E67 CRC64;

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Query Match 71.5%; Score 1954; DB 12; Length 565;
Best Local Similarity 68.6%; Pred. No. 4.3e-167;
Matches 348; Conservative 74; Mismatches 81; Indels 4; Gaps 1;
QY 1 MALMRSDMTVYLPPEVSARVYNTDYVTRISFYHAGSSRLITVGNPFYRPAGGNGQ 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 63 MALMRSSDMVYLPPEVSARVYNTDYVTRISFYHAGSSRLITVGNPFYRPAGGNGQ 122
QY 61 DIPKSAVQYRFRVQVLPDNKFGLPDINSIYPERQRLVWACAGVEIGRGOPLVGLSGH 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 123 DVPKSAFQYRFRVRLPDNKFGLPDAIYVPEARLVMAGTGVGVGGLVGLSGH 182
QY 121 PLYNKLDITENSHVSAVDTKTRDNVSVDYKOTOLCTICGCPAIGEHNTKCTACKRPL 180
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 183 PLYNKLDITENSHVSAVDTKTRDNVSVDYKOTOLCTICGCPAIGEHNTKCTACKRPL 242
QY 181 SOGDCPPELEKNTVLEEDGMDVDTGYGAMDFSTLQDTCBEPVLDICQSTICKYEDYLOMSAD 240
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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Db 243 TPQDCPPELEKNTVLEEDGMDVDTGYGAMDFSTLQDTCBEPVLDICQSTICKYEDYLOMSAD 302
QY 241 PYGDSMFELRREQLFARHFNRAGTGTVPQSLYIKTKGMRASGSCVYSPSGSIV 300
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 303 PYGDSMFELRREQLFARHFNRAGTGTVPQSLYIKTKGMRASGSCVYSPSGSIV 362
QY 301 TSDSOLFENKPYLHKAQGNNGICWNNOLFTVVTTRSTNTLTICASTOSPPVGOYDATK 360
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 363 TSEAQIFENKPYLHKAQGNNGICWNNOLFTVVTTRSTNTLTICASTOSPPVGOYDATK 422
QY 361 FKQYSHVEEYDLOFTFOLCTITLTADVNSYIHSNNSILEDWNFVPPPTSLVDYTR 420
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 423 IKEYLRHGEYDLOFTFOLCTITLTADVNSYIHSNNSILEDWNFVPPPTSLVDYTR 482
QY 421 FVQSAVITCQKXVAPTEKQDPYAKLNFVMDLKDREITLDSQPLGRKFLDIGNARRSV 542
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 483 FVQSAVITCQKXVAPTEKQDPYAKLNFVMDLKDREITLDSQPLGRKFLDIGNARRSV 542
QY 481 IGPKRKRSAPSATSSKPAKRVRR 507
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 543 VPSRKRRAPTPS---PASTKRKRK 565

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RESULT 5
081961 PRELIMINARY: PRT: 504 AA.
AC 081961:
ID 081961:
AC 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Late protein.
GN L1.
OS Human papillomavirus type 3.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10614;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
DR EMBL: X74462; CAA52475.1;
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1.
DR PRINTS: PR00865; HPVcapsidL1.
DR ProDom: PD000544; PV_capsid_L1.
SQ SEQUENCE 504 AA; 56186 MW; 4157987112159D74 CRC64;

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Query Match 70.2%; Score 1917.5; DB 12; Length 504;
Best Local Similarity 68.8%; Pred. No. 7e-164;
Matches 351; Conservative 65; Mismatches 85; Indels 9; Gaps 4;
QY 1 MALMRSDMTVYLPPEVSARVYNTDYVTRISFYHAGSSRLITVGNPFYRPAGGNGQ 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 MALMRSSDMVYLPPEVSARVYNTDYVTRISFYHAGSSRLITVGNPFYRPAGGNGQ 60
QY 61 DIPKSAVQYRFRVQVLPDNKFGLPDINSIYPERQRLVWACAGVEIGRGOPLVGLSGH 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 DIPKSAFQYRFRVRLPDNKFGLPDAIYVPEARLVMAGTGVGVGGLVGLSGH 120
QY 121 PLYNKLDITENSHVSAVDTKTRDNVSVDYKOTOLCTICGCPAIGEHNTKCTACKRPL 180
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 123 DVPKSAFQYRFRVRLPDNKFGLPDAIYVPEARLVMAGTGVGVGGLVGLSGH 182
QY 181 SOGDCPPELEKNTVLEEDGMDVDTGYGAMDFSTLQDTCBEPVLDICQSTICKYEDYLOMSAD 240
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 180 SPQDCPPELEKNTVLEEDGMDVDTGYGAMDFSTLQDTCBEPVLDICQSTICKYEDYLOMSAD 240
QY 241 PYGDSMFELRREQLFARHFNRAGTGTVPQSLYIKTKGMRASGSCVYSPSGSIV 300
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 240 PYGDSMFELRREQLFARHFNRAGTGTVPQSLYIKTKGMRASGSCVYSPSGSIV 362

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QY 298 SIYTSOSLEFNKPYWLHKAOGHNNGICWHNOLFVTVDTTSTNLITCASTQSPVPGQYD 357
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 SMATSEQLNKPFWLRRAGHNNGICWANOOLFVTVDTTSTNMTLCVSTET--SAYTD 357
QY 358 ATFEKQYSRHVEEYDLOFIFOLCTITLTADVMSTYIHSNNSILEDNMFVPPPTSLVD 417
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 358 ATFEKELRNGEEYDLOFIFOLCTITLTPELMAYLIHMNSTILEDNMFGLTLPSTLED 417
QY 418 TYRFVOSVAITCOKDAAPAKNDPDKLFTWNVDLKEKFSLIDQYPLGRKFLVQGLRR 477
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 418 TYRFVTSVAITCOKDAPEPEKODPYAKLNFWDVLDKDRFSLIDQYPLGRKFLVQGLRR 477
QY 478 KPTIGPKRSAPSATSSKPAKRVRAR 507
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 478 RSSISVKKR--SAYTTSRTAAAKRRKTK 504

RESULT 6
081958 PRELIMINARY; PRT; 503 AA.
ID 081958 AC 081958;
AC 081958;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Late protein (Fragment).
GN LI.
OS Human papillomavirus type 10.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_Taxid=10603;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9426501; Pubmed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
DR EMBL: X74465; CA52495.1; -.
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1;
DR PRINTS: PR00865; HPV_CAPSID_L1.
DR Prodom: PD000544; PV_capsid_L1; 1.
FT NON_TER 503 503
SQ SEQUENCE 503 AA; 56041 MW; 33973F92E5A79E2A CRC64;

Query Match 69.8%; Score 1909; DB 12; Length 503;
Best Local Similarity 67.9%; Pred. No. 4.1e-163;
Matches 342; Conservative 70; Mismatches 90; Indels 2; Gaps 2;

QY 1 MALMRPBDNTVYLPPPSVAVNTDDVYRTSIFTHAGSSRLITVGNPFRVPAAGGNKQ 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MALMRSSDNLVYLPPTPVSKVLSTDDVYRTNITTYAGTSRLITVGHPPPIPKSSNNKV 60
QY 61 DIPKVSAYQYRFRVOLPDPNKFGLPDNSIYNPETORLWVACAGVEIGRGOPVLGSLG 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DVPKVSAYQYRFRVRLPDPNKFGLPDARIYNPAEKLWVACGVEVGRQPLGVLGSLG 120
QY 121 PFYTKLDDTSSHAATSNVEDYRDNVSVDYKQFOLCLICAPALIGHMAKTRACKSRPL 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 PLYNKLEDFTENSNIAPGPIGODSDNINISVNDKQFOLCIICTPMGHMKGTRCPNRP- 179
QY 181 SGGDCPPLLEKNTVLEGGDNDVDTGYGAMDESTLQDTCEVPLDLCOSICGYPYLOMSAD 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 AAGDCPPLLEITPDIQDGDNDVDTGYGAMDTALQLNKSDVPLDLCOSTCKYPPDLGMAE 239
QY 241 PYGDSMFECLRRQLFARHFWNRAGTMDVTPQSLYIKGTGRASPSCSYSPSGSIY 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 PYGDSMFEYLRRLQFLARHFNRASAYGDAIPDTFLIKSNGGGADVGSAYSPTPSSSMV 299
QY 301 TTSQQLFNKPYWLHKAOGHNNGICWHNOLFVTVDTTSTNLITCASTQSPVPGQYD 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 TTSQQLFNKPYWLHKAOGHNNGICWHNOLFVTVDTTSTNLITCASTQSPVPGQYD 359
QY 361 FKQYSRVEEYDLOFIFOLCTITLTADVMSTYIHSNNSILEDNMFVPPPTTSLVDYTR 420
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Db 360 FKETLRNGEEYDLOFIFOLCTITLTADVMSTYIHSNNSILEDNMFGLTLPSTSLVDYTR 419
QY 421 FVOSVAITCOKDAAPAKNDPDKLFTWNVDLKEKFSLIDQYPLGRKFLVQGLRRKPY 480
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 420 FLSSAATCOKDDPPTPEKODPYAKLNFWDVLDKDRFSLIDQYPLGRKFLVQGLRRSRA 479
QY 481 IGPKRSAPSATSSKPAKRVRAR 504
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 480 VSVKRRPATSA--TGSTAAKRRKTK 502

RESULT 7
08UTB7 PRELIMINARY; PRT; 518 AA.
ID 08UTB7 AC 08UTB7;
AC 08UTB7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative major capsid protein LI.
GN LI.
OS Human papillomavirus type 89.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_Taxid=202250;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22079881; Pubmed=12085327;
RA Terai M., Burk R.D.;
RT "Identification and characterization of 3 novel genital human papillomaviruses by overlapping polymerase chain reaction: candidHPV9, candidHPV90, and candidHPV91."
RL J. Infect. Dis. 185:1794-1797(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Burk R.D.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF436128; AA92157.1; -.
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1;
DR PRINTS: PR00865; HPV_CAPSID_L1.
DR Prodom: PD000544; PV_capsid_L1; 1.
SQ SEQUENCE 518 AA; 58367 MW; 361232C935BE513C CRC64;

Query Match 68.4%; Score 1870; DB 12; Length 518;
Best Local Similarity 68.0%; Pred. No. 1.4e-159;
Matches 346; Conservative 72; Mismatches 75; Indels 16; Gaps 8;

QY 1 MALMRPBDNTVYLPPPSVAVNTDDVYRTSIFTHAGSSRLITVGNPFRVPAAGGNKQ 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 17 MALMRPBDGKRVYLPPTPVSKVLSTDRVYQNTNLNYYGSSRLITVGHPPYTVQVNGANKK 76
QY 61 -DIPKVSAYQYRFRVOLPDPNKFGLPDNSIYNPETORLWVACAGVEIGRGOPVLGSLG 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 77 ANIPKVSQYQYRFRRLPDPNKFGLPDASLIYNPDIERLWVACRGIEVGRQPLGVLGSLG 136
QY 120 HPEYTKLDDTSSHAATSNVEDY--RDNVSVDYKQFOLCLICAPALIGHMAKTRACKS 177
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 137 HPLYNRLDGTEN--ASLVAADVDSRDNISVDYKQFOLLIICKPPRIGHMAKTRGVCS 193
QY 178 RPLSGDCPPLLEKNTVLEGGDNDVDTGYGAMDESTLQDTCEVPLDLCOSICGYPYLOM 237
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 194 VVPQGDCCPPLQILLNTTIEDGDVETGYGAMDESKLDESEVPDIDCOSTCKYPPDYLOM 253
QY 238 SADPYGDSMFECLRRQLFARHFWNRAGTMDVTPQSLYIKGTGM--RASPGSCYVSPSP 295
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 254 AAEPIYGDCEMFECLRRQDMFRARHFNKQGVNGEPLPTLYVPGSAANNKRTLISYVAAPR 313
QY 296 SGIIVTSDQQLFNKPYWLHKAOGHNNGICWHNOLFVTVDTTSTNLITCASTQSPVPGQ 355
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 314 SGMATVSDQQLFNKPYWLHKAOGHNNGICWHNOLFVTVDTTSTNLITCASTQSGT--E 371
QY 356 YDAITKQYSRVEEYDLOFIFOLCTITLTADVMSTYIHSNNSILEDNMFVPPPTTSL 415
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Db      372 YSTREKELTTEEDLQIFOLKILHLPIMSTLHNMNPTLIDENMFVIPPSTSL 431
Qy      416 VDTYFVQSVATTCOK--DAAPAKNDPDKLKFMMVNDLKEKPSLDDQYPLGRKFLVQAG 474
Db      432 DDTYRFLNRSALTCKCKGTAPAEKPKDPYKLSFMVDLKERLSTLDQPLGRKFLQAG 491
Qy      475 LRRKPTIGRRKRSAPSATSS--KPAKR 500
Db      492 GR--PSSVPRKRAAPVSTSKAPKRKKR 518

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RESULT 8

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Q8B5X1 PRELIMINARY; PRT; 525 AA.
AC Q8B5X1;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative major capsid protein L1.
GN L1.
OS Human papillomavirus type 54.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_Taxid=37113;
RN [1]
RP SEQUENCE FROM N.A.
RA Terai M., Burk R.D.;
RT "Cervical HPV in Evolution; Genomic sequence of AE9, a subtype of
RT HPV24."
RL Submitted (OCU-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF436129; AA015434.1; -.
SQ SEQUENCE 525 AA; 58773 MW; 2BBE2F8A3DEC869B CRC64;

```

Query Match 68.1%; Score 1862.5; DB 12; Length 525;

Best local Similarity 69.0%; Pred. No. 6.7e-159; Matches 351; Conservative 57; Mismatches 84; Indels 17; Gaps 7;

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Qy      1 MALMRPSDNTVYLPPEPVARVNTDDYVTRTSIFYHAGSSRLLTGPNFYRYPAGGNGKQ 60
Db      27 MAMMRPSERKXYLPPTPVSKVYSTDEYVTRTSIYHASSRLLAVGHFVKYOK--STNKQ 85
Qy      61 DIPKSAVQYRVFVQVLPDPNFKGLPDNSIYNPETOQLVWACAGVEIGRGOPLGVLGSH 120
Db      86 SLPKSAFQYRVFVQVLPDPNFKGLPDLSLYNPEQLVWMACTGVEVGGOPLGVLGSH 145
Qy      121 PFYNNLDDTESS----HAATSNVSEVDNRDVSVDYKOTQCLITGCAPIGEMHAKGTACK 176
Db      146 PLNNKLDTEENAPKVVAGADTN-----KENVSMQKQVLCILGCTPTIGEMHAKGNLCT 200
Qy      177 SRPLSQGDCPPLLEKNTVLEDGDMVDTGYGAMDFSTLQDKCEVPLDIOQSTICKYPDYLQ 236
Db      201 PNTLAGDCPPLLELVNTYIDGDMDVIGGAMDFNALQTSKSEVPLDITATISICKYPDYLK 260
Qy      237 MSADYDGMFCLARREQLFAHFNNRAGTMDGTVPQSLYIKGTGMRASPGSCVYSPSPS 296
Db      261 MAAEYIGSLFFYLRRQEFVNHMLNRAGTMEPEVPNDLYIKSS--GAPDSIYAAPPS 318
Qy      297 GSIVTSDQLFNKPYMLHKAQGNHNGICMHNOLFVTVVDTTRSTMLTICATSQSPGQY 356
Db      319 GSMVSEYQIFNKPYMLQAGQGNNGICMGNOLFVTVVDTTRSTMLTICATQTS--QDTF 376
Qy      357 DATKQYSRHVEEYDLQIFOLCTITTLADVMSYIHSNNSILEDWNEFGVPPPTSLV 416
Db      377 NNANKEFYIRHVEEYDLQIFOLCTITTLADVMAIYHGNMPTLIDWNGIIRPATSSLE 436
Qy      417 DTYRFOVATTCQDAAPA--ENKDPYDKLKFMMVNDLKEKPSLDDQYPLGRKFLVQAGL 475
Db      437 DTYRFOVATTCQDAAPAKNEKEDPYKYAFVTVDLKERFSSDLQPLGRKFLQAGL 496
Qy      476 RRRPTIGRRKRSAPSAT--TSSKPAKRVA 502
Db      497 RRRPLRRKRAAPVSTSKAPKRKKR 525

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RESULT 9

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Q99323 PRELIMINARY; PRT; 503 AA.
AC Q99323;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Putative major capsid protein L1.
GN L1.
OS Human papillomavirus type 82.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_Taxid=129724;
RN [1]
RP SEQUENCE FROM N.A.
RA Terai M., Burk R.D.;
RT "Cervical HPV in Evolution; Genomic Sequence of IS39/AE2, a Subtype
RT of Oncogenic HPV 82 (W13B).";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF293961; AAK28456.1; -.
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; Late_protein_L1.
DR PRINTS: PR00865; HPVcapsidL1.
DR Prodom: PD000544; PV_capsid_L1; 1.
SQ SEQUENCE 503 AA; 56121 MW; F6C4F5D72BFCE93 CRC64;

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Query Match 68.1%; Score 1861; DB 12; Length 503;

Best local Similarity 66.7%; Pred. No. 8.6e-159; Matches 337; Conservative 74; Mismatches 90; Indels 4; Gaps 4;

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Qy      1 MALMRPSDNTVYLPPEPVARVNTDDYVTRTSIFYHAGSSRLLTGPNFYRYPAGGNGKQ 60
Db      1 MALMRPSDNTVYLPPEPVARVNTDEYTRITRTIYHAGSSRLITGHPFALPK--TSRA 59
Qy      61 DIPKSAVQYRVFVQVLPDPNFKGLPDNSIYNPETOQLVWACAGVEIGRGOPLGVLGSH 120
Db      60 EIPKSAFQYRVFVQVLPDPNFKGLPDPLFNPDIQLVWACAGVEVGGOPLGVLGSH 119
Qy      121 PFYNNLDDTESSHAATSNVSEVDNRDVSVDYKOTQCLITGCAPIGEMHAKGTACKSRPL 180
Db      120 PLNNKLDTEENRVANQVQDVNRDVSVDYKOTQCLITGCAPIGEMHAKGTACKSNPV 179
Qy      181 SQGDCPPLLEKNTVLEDGDMVDTGYGAMDFSTLQDKCEVPLDIOQSTICKYPDYLOMSAD 240
Db      180 PGDCPPLLELVSTIIEGDMIDTGFAMDFALQATKSPVPLDIQSVCKYPDYIKMSAD 239
Qy      241 PYGDSMFCLARREQLFAHFNNRAGTMDGTVPQSLYIKGTGMRASP--GSCVYSPSPSGSI 299
Db      240 TYGNSMFFELRRQEFARHYVRAGVGDALPDKAYIKGTGGRDPISGYSATPPSGSM 299
Qy      300 VTSDSOLFKNPYMLHKAQGNHNGICMHNOLFVTVVDTTRSTMLTICATSQSPGQYDAT 359
Db      300 VTSDSOLFKNPYMLHKAQGNHNGICMHNOLFVTVVDTTRSTMLTSTAATPSVAQTFPPT 359
Qy      360 KEKQYSRHVEEYDLQIFOLCTITTLADVMSYIHSNNSILEDWNEFGVPPPTSLVDTY 419
Db      360 NKQYIRHVEEYELQIFOLCKITLTTEMAVLIHNDSTILLEQNNFGLTLPSSALEDAY 419
Qy      420 RYVQSVATTCQDAAPAEKNDPYDKLKFMMVNDLKEKPSLDDQYPLGRKFLVQAGLRRKP 479
Db      420 RFVKNAATSCQDSDSPQAKODPLAKYKFTVTLKERFSIDLQALGRKFLQAGRA 479
Qy      480 TIGPRKRSAPSATSSKPAKRVR 504
Db      480 RRG--LKRPAVSSSSSS--AKRRVK 502

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RESULT 10

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Q91R52 PRELIMINARY; PRT; 503 AA.
AC Q91R52;

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RA Icenogle J.P., Clancy K.A., Lin S.Y.;
 RT "Sequence variation in the capsid protein genes of human
 Papillomavirus type 16 and type 31.";
 RL Virology 214:664-669(1995).
 DR EMBL: U37217: AAA92892.1: -;
 DR InterPro: IPR002210: PV_capsid_L1.
 DR Pfam: PF00500: Late_protein_L1.
 DR PRINTS: PR00865; HPVcapsidL1.
 DR PRODOM: PD000544; PV_capsid_L1: 1.
 DR SEQUENCE 505 AA; 56344 MW; 52D2D06922836F68 CRC64;

Query Match 66.9%; Score 1828; DB 12; Length 505;
 Best Local Similarity 66.1%; Pred. No. 8e-156;

Matches 332; Conservative 69; Mismatches 97; Indels 4; Gaps 3;

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QY 1 MALRPSDNTVYLLPPPSVARYVNTDDYVTRTSIFYHAGSSRLTVGNPFYRVPAAGGNKQ 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MSWLPSBATVYLLPPVPVSKVSTDEVYARNTIYHAGTSRLAVGVHFFPIKPNKKI 60

QY 61 DIPKVSAYQYRVFVQVLPDPNKFGLPDNSIYNPETQRLVMACAGVEIGRQPLGVGSGH 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 LVPRVSGIQYRVFRIYLPDPNKFGEFPTSFYNPDQRLVMACVGEVGRQPLGVGSGH 120

QY 121 PFYKKLDDTESSHAATSVSEVDVNDVSDYKQVQLICGAPAIGEHMAKGTACKSRPL 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 PLNKLKDDTENASAYANAGVDNRECISSMDYKQVQLICGKPPIGEHWKSGSCNNVAV 180

QY 181 SGGDCPPLKNTVLEGDVNDVGYGAMDFSTLQDTCCEVPLDIOQSIKYPDYLOMSAD 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 TPGDCPPLKNTVLEGDVNDVGYGAMDFSTLQANKSEVPLDICTSIKYPDYIKWSE 240

QY 241 PYGSMFECLRRQDLFARHFWNRAGTMDVYPOSLYIKGTGMRASPGSCVYSPBSGSIV 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 PYGSLFFEYLRREQMFEVHLEFNRAVAGENVDDLYIKSGPTANLASSNFFPPSGSMV 300

QY 301 TSDSOLFNRKPYWLHKAAGHNNGICMHNOLFVTVVDTTRSTNLITICASTQSPVPGQYATK 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 TSDAQIFNRKPYWLQARAGHNNGICMGNOLFVTVVDTTRSTNMSICAISTSEP-TYKNTN 359

QY 361 FKQYSRHVEEYDLOFIQOLCTITLADVMYSIHMSNSILEDWMFVGPPTTSIVDTYR 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 360 FKEYLRHGEEDLOFIQOLCTITLADVMYIHSNSTILEDWMNGIQLPPGGTLEDITYR 419

QY 421 FVQSVAITCQKDAAPAEKDPYDKLKFVNVDLKEKFSLDLDQYPLGRKFLVQAGLRKP- 479
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 420 FVTSQAIAACQKHTPPAREDEPLKRYTFWEVNLKEKFSADLDQFLGRKFLVQAGFKAPK 479

QY 480 -TIGPKRSAPSATTSSKPAKR 500
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 480 FTLGKRRK-ATPTTSTSTTTAKR 500

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RESULT 15

08B5N5 PRELIMINARY; PRT: 531 AA.

AC 08B5N5.
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Putative major capsid protein L1.
 GN L1.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 NCBI_TaxID=10581;
 NP SEQUENCE FROM N.A.
 RP Terai M., Ma Z., Burk R.D.;
 RT "Cloning and Sequencing of Non-European Human Papillomavirus (HPV)
 RT Variants Complete Genomes from Patients with Cervical Cancer by an
 RT Overlapping PCR Method.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF472509; AAO15712.1: -;

SQ SEQUENCE 531 AA; 59541 MW; F1C433C8ADA313AA CRC64;
 Query Match 66.9%; Score 1828; DB 12; Length 531;
 Best Local Similarity 66.1%; Pred. No. 8.6e-156;
 Matches 332; Conservative 69; Mismatches 97; Indels 4; Gaps 3;

```

QY 1 MALRPSDNTVYLLPPPSVARYVNTDDYVTRTSIFYHAGSSRLTVGNPFYRVPAAGGNKQ 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27 MSWLPSBATVYLLPPVPVSKVSTDEVYARNTIYHAGTSRLAVGVHFFPIKPNKKI 86

QY 61 DIPKVSAYQYRVFVQVLPDPNKFGLPDNSIYNPETQRLVMACAGVEIGRQPLGVGSGH 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 87 LVPRVSGIQYRVFRIYLPDPNKFGEFPTSFYNPDQRLVMACVGEVGRQPLGVGSGH 146

QY 121 PFYKKLDDTESSHAATSVSEVDVNDVSDYKQVQLICGAPAIGEHMAKGTACKSRPL 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 147 PLNKLKDDTENASAYANAGVDNRECISSMDYKQVQLICGKPPIGEHWKSGSCNNVAV 206

QY 181 SGGDCPPLKNTVLEGDVNDVGYGAMDFSTLQDTCCEVPLDIOQSIKYPDYLOMSAD 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 207 TPGDCPPLKNTVLEGDVNDVGYGAMDFSTLQANKSEVPLDICTSIKYPDYIKWSE 266

QY 241 PYGSMFECLRRQDLFARHFWNRAGTMDVYPOSLYIKGTGMRASPGSCVYSPBSGSIV 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 267 PYGSLFFEYLRREQMFEVHLEFNRAVAGENVDDLYIKSGPTANLASSNFFPPSGSMV 326

QY 301 TSDSOLFNRKPYWLHKAAGHNNGICMHNOLFVTVVDTTRSTNLITICASTQSPVPGQYATK 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 327 TSDAQIFNRKPYWLQARAGHNNGICMGNOLFVTVVDTTRSTNMSICAISTSEP-TYKNTN 385

QY 361 FKQYSRHVEEYDLOFIQOLCTITLADVMYSIHMSNSILEDWMFVGPPTTSIVDTYR 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 386 FKEYLRHGEEDLOFIQOLCTITLADVMYIHSNSTILEDWMFVGPPTTSIVDTYR 445

QY 421 FVQSVAITCQKDAAPAEKDPYDKLKFVNVDLKEKFSLDLDQYPLGRKFLVQAGLRKP- 479
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 446 FVTSQAIAACQKHTPPAREDEPLKRYTFWEVNLKEKFSADLDQFLGRKFLVQAGFKAPK 505

QY 480 -TIGPKRSAPSATTSSKPAKR 500
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 506 FTLGKRRK-ATPTTSTSTTTAKR 526

```

Search completed: October 17, 2003, 11:02:03
 Job time : 72.0888 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 17, 2003, 10:47:19 ; Search time 57.1488 Seconds
(without alignments)
1280.394 Million cell updates/sec

Title: US-08-913-644-4
Perfect score: 2405
Sequence: 1 MVSRRARRKRASVTDLTKT.....FIPKRRKRVYFADGFWAA 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2394.5	99.6	462	17	AAW05844
2	2317.5	96.4	21	AA23928	Human papillomavir
3	2317.5	96.4	22	AA23928	Human papillomavir
4	1973	82.0	463	22	AA23928
5	1486.5	61.8	464	22	AA23928
6	1164.5	48.4	465	22	AA23928
7	1149.5	47.8	455	22	AA23928
8	1137.5	47.3	23	AA23928	Human papillomavir
9	1134	47.2	601	17	AAW03562

10	1133.5	47.1	473	21	AA23926	Human papillomavir
11	1131.5	47.0	459	22	AA23926	Human papillomavir
12	1131	47.0	453	22	AA23926	Human papillomavir
13	1130	47.0	459	22	AA23926	Human papillomavir
14	1128.5	46.9	459	22	AA23926	Human papillomavir
15	1126	46.8	601	19	AA23926	Human papillomavir
16	1114	46.3	467	20	AA23926	Human papillomavir
17	1114	46.3	467	20	AA23926	Human papillomavir
18	108.5	17.0	469	20	AA23926	Human papillomavir
19	408.5	16.7	469	6	AA23926	Humanised bovine p
20	384.5	16.0	467	24	AA23926	Bovine papillomavir
21	292.5	12.2	154	21	AA23926	Amino acid sequenc
22	193.5	8.1	234	4	AA23926	Sequence encoded b
23	172.5	7.2	2639	22	AA23926	Novel human diagno
24	170.5	7.1	745	22	AA23926	Human testes-deriv
25	170.5	7.1	5179	22	AA23926	Human testes-deriv
26	170.5	7.1	5179	22	AA23926	Human testes-deriv
27	170	7.1	492	22	AA23926	Human testes-deriv
28	169	7.0	695	22	AA23926	Human testes-deriv
29	166	6.9	745	22	AA23926	Human testes-deriv
30	166	6.9	778	22	AA23926	Human testes-deriv
31	166	6.9	3065	24	AA23926	Human testes-deriv
32	155	6.4	540	22	AA23926	Human testes-deriv
33	155	6.4	692	22	AA23926	Human testes-deriv
34	155	6.4	717	22	AA23926	Human testes-deriv
35	155	6.4	717	22	AA23926	Human testes-deriv
36	155	6.4	717	22	AA23926	Human testes-deriv
37	155	6.4	717	22	AA23926	Human testes-deriv
38	155	6.4	717	22	AA23926	Human testes-deriv
39	155	6.4	717	22	AA23926	Human testes-deriv
40	155	6.4	717	22	AA23926	Human testes-deriv
41	155	6.4	717	22	AA23926	Human testes-deriv
42	155	6.4	1795	22	AA23926	Human testes-deriv
43	152	6.3	1296	23	AA23926	Drosophila melanog
44	152	6.3	1296	23	AA23926	Human novel polype
45	151	6.3	907	6	AA23926	Epstein-Barr virus

ALIGNMENTS

RESULT 1
ID AAW05844 standard; Protein; 462 AA.
AC AAW05844;
XX
XX 28-JAN-1997 (first entry)
XX
XX
DE Human papillomavirus type 18 L2 capsid protein.
XX
XX HPV-18; L2 gene; capsid protein; vaccine; diagnosis; vector;
XX antibody; serotyping; cervix carcinoma.
XX
XX Human papillomavirus type 18.
OS
XX
XX W09629413-A2.
XX
XX 26-SEP-1996.
XX
XX 18-MAR-1996; 96WO-US03649.
XX
XX 22-MAR-1995; 95US-0409122.
XX
XX 22-MAR-1995; 95US-0408669.
XX
XX (MERI) MERCK & CO INC.
XX
XX George HA, Hofmann KJ, Jansen KU, Joyce JS, Nepper MP;
XX WPI; 1996-443188/44.
XX N-PSDB; AAT40120.
XX
XX DNA encoding human papilloma virus 18, esp. L1 and L2 capsid

proteins - and related vectors and antibodies, useful in protective vaccines, for serotyping HPV infections and as therapeutic agents

Claim 2; Fig 3; 46pp; English.

The L2 minor capsid protein (AA05844) of human papillomavirus type 18 (HPV18) has a mol. wt. of 55-60 kDa and is thought to be internal to the L1 major capsid protein (AA05843) in the viral capsomere. Its amino acid sequence was deduced from a genomic clone (AAT40120) isolated from human cervical carcinoma SW756 cells. Recombinant L2 and L1 proteins can be produced in transformed host cells and used in vaccines for protection against HPV18; this HPV type is associated with invasive carcinomas of the cervix, vagina, vulva and anal canal. Virus-like particles composed of recombinant L1+L2 can be produced in yeast for use as vaccines.

Sequence 462 AA;

Query Match 99.6%; Score 2394.5; DB 17; Length 462;
Best Local Similarity 99.8%; Pred. No. 2.7e-171;
Matches 461; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

QY 1 MSHRAARRKRASTYDLYKTKCKQSGTQPSDVNVEGTTADKLQSSLGIFLGAGIG 60
DB 1 MSHRAARRKRASTYDLYKTKCKQSGTQPSDVNVEGTTADKLQSSLGIFLGAGIG 60
QY 61 TGSSTGRTGYIPLGGSNTYVDGPTRPVPIEVPGETDPSIVTLIEDSSVYTSGARPP 120
DB 61 TGSSTGRTGYIPLGGSNTYVDGPTRPVPIEVPGETDPSIVTLIEDSSVYTSGARPP 120
QY 121 TFGTSGFDITSACTTTPAVLDITPSSVSISTNTNPAFSDPSIIEVPQTEVSGNV 180
DB 121 TFGTSGFDITSACTTTPAVLDITPSSVSISTNTNPAFSDPSIIEVPQTEVSGNV 180
QY 121 TFGTSGFDITSACTTTPAVLDITPSSVSISTNTNPAFSDPSIIEVPQTEVSGNV 180
DB 121 TFGTSGFDITSACTTTPAVLDITPSSVSISTNTNPAFSDPSIIEVPQTEVSGNV 180
QY 181 FVGPTSGTHGEIEIPLOTFASSGTGEEPISTPLPVRRVAGRLYSRAVOQSVANPE 240
DB 181 FVGPTSGTHGEIEIPLOTFASSGTGEEPISTPLPVRRVAGRLYSRAVOQSVANPE 240
QY 241 FLTRPSSLITYDNDNAFEPVDITLFEPRSNVPPDSDFMDIIRLHRPALTSRGTFRSRLG 300
DB 241 FLTRPSSLITYDNDNAFEPVDITLFEPRSNVPPDSDFMDIIRLHRPALTSRGTFRSRLG 300
QY 301 QRATMFTRSQTQIGARVHFYHDISPAPSEYIELQPLVSATEDNGLFDIYADDIDPAMP 360
DB 301 QRATMFTRSQTQIGARVHFYHDISPAPSEYIELQPLVSATEDNGLFDIYADDIDPAMP 360
QY 361 VPSRPTSSAVSTYSPITSSASSYNTVPLTSSMDVPVYTGPDITLP-TSWPVTSPPT 419
DB 361 VPSRPTSSAVSTYSPITSSASSYNTVPLTSSMDVPVYTGPDITLP-TSWPVTSPPT 419
QY 420 APASTQYIGIHGTHYILMPLYYFIPKKRKRPVFFADGFVAA 461
DB 420 APASTQYIGIHGTHYILMPLYYFIPKKRKRPVFFADGFVAA 461

```

RESULT 2

AA05844 standard; protein: 462 AA.

AA05844;

18-JAN-2001 (first entry)

Human papillomavirus 18 L2 protein SEQ ID NO:4.

Human papillomavirus; HPV16; HPV18; L1 protein; L2 protein; antiviral;

vaccine; immunisation; immune response; infection; diagnosis.

Human papillomavirus.

WO200054730-A2.

21-SEP-2000.

08-MAR-2000; 2000WO-US06017.
18-MAR-1999; 99US-0125208.
12-AUG-1999; 99US-0148544.
(HARD) HARVARD COLLEGE.
(HARR) HARRISON S.
(CHEN) CHEN X.
Harrison S, Chen X;
WPI; 2000-628165/60.
Composition comprising multimer of human papillomavirus L1 protein
useful as vaccines against human papillomavirus infection, as
diagnostic tools for detecting presence of the virus in biological
samples -
Disclosure; Page 31; 31pp; English.

The present invention describes a composition (I) comprising a multimer of human papillomavirus (HPV) L1 protein (II) which is truncated at its amino terminus. (I) has antiviral activity and can be used in the production of a vaccine. (I) comprising a multimer of HPV L1 protein (a T=1 icosahedral particle comprising a pentamer of L1 protein, one of which comprises HPV L2 protein) when administered induces an immune response against the L1 protein in the humans and is thus useful for immunising the humans against HPV. (I) is thus useful as vaccines against human papillomavirus infection, as diagnostic tools for detecting the presence of HPV in biological samples and as tools for mapping receptor interactions. The present sequence represents an HPV18 L2 protein sequence which is used in the exemplification of the present invention.

Sequence 462 AA;

Query Match 96.4%; Score 2317.5; DB 21; Length 462;
Best Local Similarity 96.8%; Pred. No. 1.6e-165;
Matches 447; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

```

QY 1 MSHRAARRKRASTYDLYKTKCKQSGTQPSDVNVEGTTADKLQSSLGIFLGAGIG 60
DB 1 MSHRAARRKRASTYDLYKTKCKQSGTQPSDVNVEGTTADKLQSSLGIFLGAGIG 60
QY 61 TGSSTGRTGYIPLGGSNTYVDGPTRPVPIEVPGETDPSIVTLIEDSSVYTSGARPP 120
DB 61 TGSSTGRTGYIPLGGSNTYVDGPTRPVPIEVPGETDPSIVTLIEDSSVYTSGARPP 120
QY 121 TFGTSGFDITSACTTTPAVLDITPSSVSISTNTNPAFSDPSIIEVPQTEVSGNV 180
DB 121 TFGTSGFDITSACTTTPAVLDITPSSVSISTNTNPAFSDPSIIEVPQTEVSGNV 180
QY 121 TFGTSGFDITSACTTTPAVLDITPSSVSISTNTNPAFSDPSIIEVPQTEVSGNV 180
DB 121 TFGTSGFDITSACTTTPAVLDITPSSVSISTNTNPAFSDPSIIEVPQTEVSGNV 180
QY 181 FVGPTSGTHGEIEIPLOTFASSGTGEEPISTPLPVRRVAGRLYSRAVOQSVANPE 240
DB 181 FVGPTSGTHGEIEIPLOTFASSGTGEEPISTPLPVRRVAGRLYSRAVOQSVANPE 240
QY 241 FLTRPSSLITYDNDNAFEPVDITLFEPRSNVPPDSDFMDIIRLHRPALTSRGTFRSRLG 300
DB 241 FLTRPSSLITYDNDNAFEPVDITLFEPRSNVPPDSDFMDIIRLHRPALTSRGTFRSRLG 300
QY 301 QRATMFTRSQTQIGARVHFYHDISPAPSEYIELQPLVSATEDNGLFDIYADDIDPAMP 360
DB 301 QRATMFTRSQTQIGARVHFYHDISPAPSEYIELQPLVSATEDNGLFDIYADDIDPAMP 360
QY 361 VPSRPTSSAVSTYSPITSSASSYNTVPLTSSMDVPVYTGPDITLP-TSWPVTSPPT 419
DB 361 VPSRPTSSAVSTYSPITSSASSYNTVPLTSSMDVPVYTGPDITLP-TSWPVTSPPT 419
QY 420 APASTQYIGIHGTHYILMPLYYFIPKKRKRPVFFADGFVAA 461
DB 420 APASTQYIGIHGTHYILMPLYYFIPKKRKRPVFFADGFVAA 461

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RESULT 3
AAB98430
ID   AAB98430 standard; Protein; 462 AA.
XX
AC   AAB98430;
XX
DT   22-AUG-2001 (first entry)
XX
DE   Human papillomavirus protein HPV18 L2.
XX
KM   Human papillomavirus; human leukocyte antigen; HLA; immune response;
KW   HPV; epitope; T cell; identification; vaccine; infection; genital wart;
KW   neoplastic growth; antiviral.
XX
OS   Human papillomavirus.
XX
PN   WO200141799-A1.
XX
PD   14-JUN-2001.
XX
PF   11-DEC-2000; 2000WO-US33549.
XX
PR   10-DEC-1999; 99US-0172705.
XX
PR   15-AUG-2000; 2000US-0641528.
XX
PA   (EPI-M-) EPIIMUNE INC.
XX
PI   Sette A, Sidney J, Southwood S, Chesnut R, Cells E, Grey HM;
XX
DR   WPI, 2001-381497/40.
XX
PT   An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT   treating HPV infections -
XX
PS   Disclosure: Page 22-23; 756pp; English.
XX
CC   The present invention describes an isolated prepared human papillomavirus
CC   (HPV) epitope (I). (I) has antiviral activity, and can be used in
CC   vaccine production. Peptides and corresponding nucleic acid compositions
CC   from the present invention are useful for stimulating an immune response
CC   to HPV by stimulating the production of CTL or HTL responses,
CC   specifically in the treatment or prophylaxis of HPV infection, in persons
CC   who have not manifested symptoms e.g. genital warts or neoplastic growth.
CC   The peptides can also be used in a tetramer staining assay to assess
CC   peripheral blood mononuclear cells for the presence of antigen-specific
CC   CTLs following exposure to a pathogen or immunogen, and as reagents to
CC   evaluate immune recall responses or evaluate the efficacy of a vaccine.
CC   The vaccine compositions are useful for removing warts or treating HPV
CC   infections. The epitopes for inclusion in an epitope-base vaccine may
CC   be selected from conserved regions of viral or tumour-associated
CC   antigens, which reduces the likelihood of escape mutants, also
CC   immunosuppressive epitopes that may be present in whole antigens can be
CC   avoided with the use of epitope-base vaccines. An additional advantage
CC   is the ability to combine selected epitopes (CTL and HTL) and to modify
CC   the composition of the epitopes achieving enhanced immunogenicity, the
CC   major benefit of the vaccine is that is safe and efficacious. AAB98391
CC   to AAB98477 represent polypeptide sequences used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 462 AA:
Query Match 96.4%; Score 2317.5; DB 22; Length 462;
Best Local Similarity 96.8%; Pred. No. 1.6e-165;
Matches 447; Conservative 5; Mismatches 9; Indels 1; Gaps 1;
OY 1 MVSRAARRKRSYVDLKYTKCKSGTSPDVNKNKVEGTTLAKTLLIOWSSIGFLGIGIG 60
DB 1 MVSRAARRKRSYVDLKYTKCKSGTSPDVNKNKVEGTTLAKTLLIOWSSIGFLGIGIG 60
OY 61 TGSGTGRTGYIPLGSRNTVVDGPTRPVVEIEFVGFTDPSIVTLIEDSSVYTSGARPP 120
DB 61 TGSGTGRTGYIPLGSRNTVVDGPTRPVVEIEFVGFTDPSIVTLIEDSSVYTSGARPP 120
DB 61 TGSGTGRTGYIPLGSRNTVVDGPTRPVVEIEFVGFTDPSIVTLIEDSSVYTSGARPP 120

```

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OY 121 TFGTSGFDITAGCTTTPAVLDITPSSSVSISTNFTNPAPSDPSIIEVPTGEGVSGNV 180
DB 121 TFGTSGFDITAGCTTTPAVLDITPSSSVSISTNFTNPAPSDPSIIEVPTGEGVSGNV 180
OY 181 FVGTPTSGHGEYEEIPLQFASSGGEEPISSPTPLTVNRVAGPRLXSAAYQVAVNPE 240
DB 181 FVGTPTSGHGEYEEIPLQFASSGGEEPISSPTPLTVNRVAGPRLXSAAYQVAVNPE 240
OY 241 FLTRPSLLTYNPAFEPVDITLTFEPRSNVDPDSFMDIIRLHRPALTSRGTFFSRIG 300
DB 241 FLTRPSLLTYNPAFEPVDITLTFEPRSNVDPDSFMDIIRLHRPALTSRGTFFSRIG 300
OY 301 QRAVFTNSGTQIGARVHFYHDIISPAFPEYIEIQLPVASATDNGLFYDADIDPAMP 360
DB 301 QRAVFTNSGTQIGARVHFYHDIISPAFPEYIEIQLPVASATDNGLFYDADIDPAMP 360
OY 361 VPSRPTSSAVSTYSPITSSASYSNVTPLSSMDVPYTGPDITLP-PTSVWPIVSP 419
DB 361 VPSRPTSSAVSTYSPITSSASYSNVTPLSSMDVPYTGPDITLP-PTSVWPIVSP 419
OY 420 APASTQYIGIHGTHYIWPPLYFYFIPKKRRVPYFFADGFVAA 461
DB 420 APASTQYIGIHGTHYIWPPLYFYFIPKKRRVPYFFADGFVAA 461
OY 421 APASTQYIGIHGTHYIWPPLYFYFIPKKRRVPYFFADGFVAA 462
DB 421 APASTQYIGIHGTHYIWPPLYFYFIPKKRRVPYFFADGFVAA 462

RESULT 4
AAB98443
ID   AAB98443 standard; Protein; 463 AA.
XX
AC   AAB98443;
XX
DT   22-AUG-2001 (first entry)
XX
DE   Human papillomavirus protein HPV45 L2.
XX
KM   Human papillomavirus; human leukocyte antigen; HLA; immune response;
KW   HPV; epitope; T cell; identification; vaccine; infection; genital wart;
KW   neoplastic growth; antiviral.
XX
OS   Human papillomavirus.
XX
PN   WO200141799-A1.
XX
PD   14-JUN-2001.
XX
PF   11-DEC-2000; 2000WO-US33549.
XX
PR   10-DEC-1999; 99US-0172705.
XX
PR   15-AUG-2000; 2000US-0641528.
XX
PA   (EPI-M-) EPIIMUNE INC.
XX
PI   Sette A, Sidney J, Southwood S, Chesnut R, Cells E, Grey HM;
XX
DR   WPI, 2001-381497/40.
XX
PT   An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT   treating HPV infections -
XX
PS   Disclosure: Page 25; 756pp; English.
XX
CC   The present invention describes an isolated prepared human papillomavirus
CC   (HPV) epitope (I). (I) has antiviral activity, and can be used in
CC   vaccine production. Peptides and corresponding nucleic acid compositions
CC   from the present invention are useful for stimulating an immune response
CC   to HPV by stimulating the production of CTL or HTL responses,
CC   specifically in the treatment or prophylaxis of HPV infection, in persons
CC   who have not manifested symptoms e.g. genital warts or neoplastic growth.
CC   The peptides can also be used in a tetramer staining assay to assess
CC   peripheral blood mononuclear cells for the presence of antigen-specific
CC   CTLs following exposure to a pathogen or immunogen, and as reagents to
CC   evaluate immune recall responses or evaluate the efficacy of a vaccine.
CC   The vaccine compositions are useful for removing warts or treating HPV

```

CC infections. The epitopes for inclusion in an epitope-base vaccine may
 CC be selected from conserved regions of viral or tumour-associated
 CC antigens, which reduces the likelihood of escape mutants, also
 CC immunosuppressive epitopes that may be present in whole antigens can be
 CC avoided with the use of epitope-base vaccines. An additional advantage
 CC is the ability to combine selected epitopes (CTL and HTL) and to modify
 CC the composition of the epitopes achieving enhanced immunogenicity, the
 CC major benefit of the vaccine is that is safe and efficacious. AAB98391
 CC to AAB98477 represent polypeptide sequences used in the exemplification
 CC of the present invention.

XX Sequence 463 AA;

Query Match 82.0%; Score 1973; DB 22; Length 463;
 Best Local Similarity 81.7%; Pred. No. 1,1e-139;
 Matches 379; Conservative 33; Mismatches 48; Indels 4; Gaps 3;

QY 1 MSHRARRRRASVTDLYKTKCKOSGTCPSDVNVEGTTADKLQWSSIGIFLGIGIG 60
 DB 1 MSHRARRRRASVTDLYKTKCKOSGTCPSDVNVEGTTADKLQWSSIGIFLGIGIG 60
 QY 61 TSGGTGRTGYIPLGSRNTVDVGPTRPVYIEPVGPTDPSITVLTLEDSSVTSAGARP 120
 DB 61 TSGGTGRTGYIPLGSRNTVDVGPTRPVYIEPVGPTDPSITVLTLEDSSVTSAGARP 120
 QY 121 TFGTSGFDITSAGTTTAVLDITPSTSVSISTNTNPAFSDPSITIEVPQTEVSGNV 180
 DB 121 TFGTSGFDITSAGTTTAVLDITPSTSVSISTNTNPAFSDPSITIEVPQTEVSGNV 180
 QY 181 FVCGPTSGTGYEIPLOTFASSGTEPISPTPLPVRRVAGRLTSRAVQGVANPE 240
 DB 181 FVCGPTSGTGYEIPLOTFASSGTEPISPTPLPVRRVAGRLTSRAVQGVANPE 240
 QY 241 FLTPSSLTLYDNPAPFVDITLTFEPRSNVPSDFMDIIRLARPALTSRGTVFSGRLG 300
 DB 241 FLTPSSLTLYDNPAPFVDITLTFEPRSNVPSDFMDIIRLARPALTSRGTVFSGRLG 300
 QY 301 ORATMFRSGTQIGARVHFHDISPIAPSEYIELOLVGATEENGFLPDYADIDPAMP 360
 DB 301 ORATMFRSGTQIGARVHFHDISPIAPSEYIELOLVGATEENGFLPDYADIDPAMP 360
 QY 361 VPSRPTSSAVSYSPYSS--ASSYSNVYPLTSSMDVYVYVGTDLTPP--TSWPIVS 417
 DB 361 VPSRPTSSAVSYSPYSS--ASSYSNVYPLTSSMDVYVYVGTDLTPP--TSWPIVS 417
 QY 418 PLTAPASTQYIGHGTHTYLLPLLYFTPKRRKRVDFEADGFVAA 461
 DB 418 PLTAPASTQYIGHGTHTYLLPLLYFTPKRRKRVDFEADGFVAA 461
 QY 420 PTNASTTYYIGHGTQYLLMPYVYFFPKRRKRIPYFFADGFVAA 463
 DB 420 PTNASTTYYIGHGTQYLLMPYVYFFPKRRKRIPYFFADGFVAA 463

RESULT 5

AAB98455 standard; Protein: 464 AA.

XX AAB98455;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Human papillomavirus protein HPV56 L2.
 XX
 KW Human papillomavirus; human leukocyte antigen; HLA; immune response;
 KM HPV; epitope; T cell; identification; vaccine; infection; genital wart;
 XX neoplastic growth; antiviral.
 OS Human papillomavirus.
 XX
 PN MO20014179-A1.
 PD 14-JUN-2001.
 XX
 PF 11-DEC-2000; 2000WO-US33549.
 XX
 PR 10-DEC-1999; 99US-0172705.

PR 15-AUG-2000; 2000US-0641528.
 XX
 PA (EPIM-) EPIMUNE INC.
 PI Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;
 DR WPI; 2001-381497/40.
 XX

PT An isolated human papilloma virus (HPV) epitope, useful in vaccines for
 XX treating HPV infections -
 XX

PS Disclosure; Page 27; 756pp; English.

CC The present invention describes an isolated prepared human papillomavirus
 CC (HPV) epitope (I). (I) has antiviral activity, and can be used in
 CC vaccine production. Peptides and corresponding nucleic acid compositions
 CC from the present invention are useful for stimulating an immune response
 CC to HPV by stimulating the production of CTL or HTL responses,
 CC specifically in the treatment or prophylaxis of HPV infection, in persons
 CC who have not manifested symptoms e.g. genital warts or neoplastic growth.
 CC The peptides can also be used in a tetramer staining assay to assess
 CC peripheral blood mononuclear cells for the presence of antigen-specific
 CC CTLs following exposure to a pathogen or immunogen, and as reagents to
 CC evaluate immune recall responses or evaluate the efficacy of a vaccine.
 CC The vaccine compositions are useful for removing warts or treating HPV
 CC infections. The epitopes for inclusion in an epitope-base vaccine may
 CC be selected from conserved regions of viral or tumour-associated
 CC antigens, which reduces the likelihood of escape mutants, also
 CC immunosuppressive epitopes that may be present in whole antigens can be
 CC avoided with the use of epitope-base vaccines. An additional advantage
 CC is the ability to combine selected epitopes (CTL and HTL) and to modify
 CC the composition of the epitopes achieving enhanced immunogenicity, the
 CC major benefit of the vaccine is that is safe and efficacious. AAB98391
 CC to AAB98477 represent polypeptide sequences used in the exemplification
 CC of the present invention.

XX Sequence 464 AA;

Query Match 61.8%; Score 1486.5; DB 22; Length 464;
 Best Local Similarity 61.1%; Pred. No. 3.4e-103;
 Matches 284; Conservative 68; Mismatches 108; Indels 5; Gaps 4;

QY 1 MSHRARRRRASVTDLYKTKCKOSGTCPSDVNVEGTTADKLQWSSIGIFLGIGIG 60
 DB 1 MSHRARRRRASVTDLYKTKCKOSGTCPSDVNVEGTTADKLQWSSIGIFLGIGIG 60
 QY 61 TSGGTGRTGYIPLGSRNTVDVGPTRPVYIEPVGPTDPSITVLTLEDSSVTSAGARP 120
 DB 61 TSGGTGRTGYIPLGSRNTVDVGPTRPVYIEPVGPTDPSITVLTLEDSSVTSAGARP 120
 QY 121 TFGTSGFDITSAGTTTAVLDITPSTSVSISTNTNPAFSDPSITIEVPQTEVSGNV 180
 DB 121 TFGTSGFDITSAGTTTAVLDITPSTSVSISTNTNPAFSDPSITIEVPQTEVSGNV 180
 QY 181 FVCGPTSGTGYEIPLOTFASSGTEPISPTPLPVRRVAGRLTSRAVQGVANPE 240
 DB 181 FVCGPTSGTGYEIPLOTFASSGTEPISPTPLPVRRVAGRLTSRAVQGVANPE 240
 QY 241 FLTPSSLTLYDNPAPFVDITLTFEPRSNVPSDFMDIIRLARPALTSRGTVFSGRLG 300
 DB 241 FLTPSSLTLYDNPAPFVDITLTFEPRSNVPSDFMDIIRLARPALTSRGTVFSGRLG 300
 QY 301 ORATMFRSGTQIGARVHFHDISPIAPSEYIELOLVGATEENGFLPDYADIDPAMP 360
 DB 301 ORATMFRSGTQIGARVHFHDISPIAPSEYIELOLVGATEENGFLPDYADIDPAMP 360
 QY 361 VPSRPTSSAVSYSPYSS--ASSYSNVYPLTSSMDVYVYVGTDLTPP--TSWPIVS 417
 DB 361 VPSRPTSSAVSYSPYSS--ASSYSNVYPLTSSMDVYVYVGTDLTPP--TSWPIVS 417
 QY 418 PLTAPASTQYIGHGTHTYLLPLLYFTPKRRKRVDFEADGFVAA 461
 DB 418 PLTAPASTQYIGHGTHTYLLPLLYFTPKRRKRVDFEADGFVAA 461
 QY 420 PTNASTTYYIGHGTQYLLMPYVYFFPKRRKRIPYFFADGFVAA 464
 DB 420 PTNASTTYYIGHGTQYLLMPYVYFFPKRRKRIPYFFADGFVAA 464

RESULT 6
AAB98437
ID AAB98437 standard; Protein; 466 AA.
XX
XX AAB98437;
XX
XX 22-AUG-2001 (first entry)
XX
DE Human papillomavirus protein HPV31 L2.
XX
XX Human papillomavirus; human leukocyte antigen; HLA; immune response;
KW HPV; epitope; T cell; identification; vaccine; infection; genital wart;
KM neoplastic growth; antiviral.
XX
OS Human papillomavirus.
XX
PN WO200141799-A1.
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000MO-US33549.
XX
PR 10-DEC-1999; 9905-0172705.
PR 15-AUG-2000; 200005-0641528.
XX
PA (EPIW-) EPIMUNE INC.
PI Sette A, Sidney J, Southwood S, Chesnut R, Cells E, Grey HM;
PI WPI; 2001-381497/40.
DR
XX
XX An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT treating HPV infections -
PT
XX
XX Disclosure; Page 24; 756pp; English.
XX
XX The present invention describes an isolated prepared human papillomavirus
CC (HPV) epitope (I). (I) has antiviral activity, and can be used in
CC vaccine production. Peptides and corresponding nucleic acid compositions
CC from the present invention are useful for stimulating an immune response
CC to HPV by stimulating the production of CTL or HTL responses,
CC specifically in the treatment or prophylaxis of HPV infection, in persons
CC who have not manifested symptoms e.g. genital warts or neoplastic growth.
CC The peptides can also be used in a tetramer staining assay to assess
CC peripheral blood mononuclear cells for the presence of antigen-specific
CC CTLs following exposure to a pathogen or immunogen, and as reagents to
CC evaluate immune recall responses or evaluate the efficacy of a vaccine.
CC The vaccine compositions are useful for removing warts or treating HPV
CC infections. The epitopes for inclusion in an epitope-base vaccine may
CC be selected from conserved regions of viral or tumour-associated
CC antigens, which reduces the likelihood of escape mutants, also
CC immunosuppressive epitopes that may be present in whole antigens can be
CC avoided with the use of epitope-base vaccines. An additional advantage
CC is the ability to combine selected epitopes (CTL and HTL) and to modify
CC the composition of the epitopes achieving enhanced immunogenicity, the
CC major benefit of the vaccine is that is safe and efficacious. AAB98391
CC to AAB98477 represent polypeptide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 466 AA;
XX
Query Match 48.4%; Score 1164.5; DB 22; Length 466;
Best Local Similarity 50.6%; Pred. No. 4.8e-79;
Matches 247; Conservative 77; Mismatches 115; Indels 49; Gaps 14;
QY 1 MSHRAARR-KRASVTDLYKTCQSGTCSGVVNVKVEGTTADKILQWSSLGIFLGIGI 59
1
DB 1 MSHKSTKTKRKASATQYTCKAAGTCSVDVPIKIEHTIADQILRYGSMGVFGSLGI 60
1
QY 60 GCGSGGRTGYPLDGRSTYDVG-PTRPPVIVPEVGTDTSTYLLFDDSVYVSGAP 118
1 1

DB 61 GCGSGGRTGYPLDGRSTYVSEASIPTRPPVSDVDPDLDSIVLSVEGIVDVGAP 120
QY 119 RPT--FTGSGFDITAGTTTTPAVLDITPSTSVSISTNTFTNPAFSDPSIIEVQGTGEV 176
1
DB 121 APIHPPTTSGFIATTAOTTPALDVT-----SVST--HEMPTTDDSVLQPPRPAT 172
1
QY 177 SGNVFVGTPTSGTHGYEELPLQTFPAGSGTGEPISSPTLPYVRVAGPRLYSRVQGVSV 236
1
DB 173 SCHLLSSSSISYHNNEEIPMDTFIVSTNNENITSTPIGVRRPARLGLYSKATQGVAV 232
1
QY 237 ANPEFLTRPSLITTYNPAFEVY--DTYLFEEFSN--VPDSEFMILRHRALTSRSG 292
1
DB 233 IDTFLSAPKQTLTYTNPATVETVNAESELFSNTSHNAPDPELDIALHRPALYSRRN 292
1
QY 293 TVFESRLGORATFTFSGTOIGARVHEHDISPIASPEYIELQPL-----VSATEDNGI 347
1
DB 293 TVRYSRLGNKQTLRTSGATIGARVHYIIDISSINAGESIEQPLGASITTTSTANDGL 352
1
QY 348 FDIYAD-----DIDPAMPVPSRPTTSSAVSTYSPTISSASSYSNVTVPLTSSMD 396
1
DB 353 YDIYADTDFTVDPATHNVSPSTAVQS---TSVSAVYPT-----NTVPLSTGFD 400
1
QY 397 VPYITGPDITL--PPTSWMPVSPPTAPASTQY-IGIHGHYIYIPLIYFIPKRRKVPYF 453
1
DB 401 IPIFSGPDVPEIHAPOVEFE--PLAPTPQVSIIFVGGDFDLPSTYMLKRRKRKVSXF 458
1
QY 454 FADGFVAA 461
1
DB 459 FTDVSVAA 466
1
RESULT 7
AAB98416
ID AAB98416 standard; Protein; 455 AA.
XX
XX AAB98416;
XX
XX 22-AUG-2001 (first entry)
XX
XX Human papillomavirus protein HPV11 L2.
DE
XX
XX Human papillomavirus; human leukocyte antigen; HLA; immune response;
KW HPV; epitope; T cell; identification; vaccine; infection; genital wart;
KM neoplastic growth; antiviral.
XX
OS Human papillomavirus.
XX
PN WO200141799-A1.
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000MO-US33549.
XX
PR 10-DEC-1999; 9905-0172705.
PR 15-AUG-2000; 200005-0641528.
XX
PA (EPIW-) EPIMUNE INC.
PI Sette A, Sidney J, Southwood S, Chesnut R, Cells E, Grey HM;
PI WPI; 2001-381497/40.
DR
XX
XX An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT treating HPV infections -
PT
XX
XX Disclosure; Page 20; 756pp; English.
XX
XX The present invention describes an isolated prepared human papillomavirus
CC (HPV) epitope (I). (I) has antiviral activity, and can be used in
CC vaccine production. Peptides and corresponding nucleic acid compositions
CC from the present invention are useful for stimulating an immune response
CC to HPV by stimulating the production of CTL or HTL responses,
CC specifically in the treatment or prophylaxis of HPV infection, in persons

CC who have not manifested symptoms e.g. genital warts or neoplastic growth.
 CC The peptides can also be used in a tetramer staining assay to assess
 CC peripheral blood mononuclear cells for the presence of antigen-specific
 CC CTLs following exposure to a pathogen or immunogen, and as reagents to
 CC evaluate immune recall responses or evaluate the efficacy of a vaccine.
 CC The vaccine compositions are useful for removing warts or treating HPV
 CC infections. The epitopes for inclusion in an epitope-base vaccine may
 CC be selected from conserved regions of viral or tumour-associated
 CC antigens, which reduces the likelihood of escape mutants, also
 CC immunosuppressive epitopes that may be present in whole antigens can be
 CC avoided with the use of epitope-base vaccines. An additional advantage
 CC is the ability to combine selected epitopes (CTL and HTL) and to modify
 CC the composition of the epitopes achieving enhanced immunogenicity, the
 CC major benefit of the vaccine is that is safe and efficacious. AAB98391
 CC to AAB98477 represent polypeptide sequences used in the exemplification
 CC of the present invention.

SO Sequence 455 AA;

Query Match 47.88; Score 1149.5; DB 22; Length 455;

Best Local Similarity 51.68; Pred. No. 6.2e-78;

Matches 239; Conservative 70; Mismatches 137; Indels 17; Gaps 10;

5 RAARKRASVYDLYKTCQSGTSDVYNNKVEGFTLADKILQMSLIGLIGTGSG 64
 4 RAARKRASATOLQTCATGTCPPDVPKVEHTTADQILKWSLGVFEGGLIGTGAG 63
 65 TGGRTGYIPLGGRSNTVVDGP--TRPVVIEPVGPTDPSITLLIEDSSVTVSGAPRPTFT 123
 64 SCGRAGYIPLGSSPKPAITGCPARPPVLEVPAPSDPSIVSLIEESALINAGAPVEVPP 123
 124 CTSGFDITSAGTTPPAVLIDTPSSVSISTNTNPAFSDPSIIEVPQTEVSGNVFVG 183
 124 TGGFTTSSSTTPALD---SVTNHTTTSVFQNPLETPSVYIQDPPVEASGHLIIS 180
 184 TPRTGTYGERIPLOTFASSGTCGEPISSPTLPVRRVAGPR--LYSRAYQGVANDEF 241
 181 APRTTSGHVEDIPEDTIVVSSSDGSPSSITPLP--KAPRRVGLYSKALQOVVTPDAF 238
 242 LTRPSSLTVDNPAFEVDVTLTFEPRS--NVPSDFMDIIRLHRPALTSRGTRESRL 299
 239 LSTPQRLVTVYDNPVEGEDVSLQFTHESSIHNAPEAEFMDIIRLHRPALTSRGLVRSRI 298
 300 GORATMETRSQTQIGARVHFYHNDISPTAPSEYIELQPLVSATEDNGLFDIYADDIDPAM 359
 299 GORSMTRSGQIHGARVHFQDISPVQAEEIELEPLVAA--ENDTFDIYAEFPD-I 355
 360 PVPSRPTTSSAVSYSPTISSASSSVNVTVPVLTSSMDVPVYTGPDITLPTSVMPVSPPT 419
 356 PDVQHSVTQSYLSTFNLTLS-QSMGNTVPLSLPSDMFVQSGPDITFPPTASMGTPSPSPV 414
 420 APA-STQYIGIHGTHYVLMPLYYFIPKKRRKVPYFEADGEVAA 461
 415 TPALPTGPVFTVTSDFLHPTWYFARRRRKRRIPLFTD--VAA 455

RESULT 8

ABB77480 ID ABB77480 standard; Protein; 473 AA.

AC ABB77480;

DT 22-JUL-2002 (first entry)

DE HPV16-L2.

KW Human papilloma virus; HPV; HPV16-L1; HPV16-L2; vaccine; cervical cancer;

XX HPV16-L1; cytosolic; virucide.

XX Human papillomavirus.

XX OS

XX

XX

XX

XX

XX

XX

PD 16-MAY-2002.

XX 19-SEP-2001; 2001WO-DE03618.

XX 09-NOV-2000; 2000DE-105545.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PA (IPK-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.

PI Mueller M, Leder C, Kleinschmidt J, Sonnewald U, Blomelt S;

XX WPI: 2002-426950/45.

XX N-PSDB: ABL58978.

PT New DNA sequences encoding human papilloma virus L1 or L2 protein,

PT useful in vaccines, are optimized for high-level expression in

XX eukaryotic cells

XX Claim 1; Fig 7; 39pp; German.

The invention relates to DNA sequences (I) that encode human papilloma virus (HPV) L1 protein (ABL58976, ABL58977) or L2 protein (ABL58978) or proteins with the biological activity of L1 and L2. Expression vectors containing (I) or a similar sequence encoding an L1/L2 fusion protein (ABL58979-ABL58981) and the proteins encoded by them (ABB77478-ABB77483), are also useful for recombinant production of L1 and L2 proteins. (I) are optimised for codon usage in eukaryotic cells and provide high yields of L1/L2 or their fusions, without the use of viral vectors.

SO Sequence 473 AA;

Query Match 47.38; Score 1137.5; DB 23; Length 473;

Best Local Similarity 49.48; Pred. No. 5.2e-77;

Matches 238; Conservative 72; Mismatches 131; Indels 41; Gaps 12;

6 AARKRASVYDLYKTCQSGTSDVYNNKVEGFTLADKILQMSLIGLIGTGSGT 65
 7 AKRTKRASATOLQYXTCQAGTCPPDIIPKVEGKTIADQIIQYSGMGVFGGLIGTGSGT 66
 66 GGRGTGYIPLGGRSNTVVD--VGTRPVVIEPVGPTDPSITLLIEDSSVTVSGAPR--PTF 122
 67 GGRGTGYIPLGTRPPATADTILAPVAPPLTVDPVGRSDPSIVSLVEETFIAGAPTSVPSI 126
 123 -TGSGFDITSAGTTPPAVLIDTPSSVSISTNTNPAFSDPSIIEVPQTEVSGNVF 181
 127 PPDVSGFSTTSFTTPALIDINTVTV---TTHNNPFTDPSVQLPPTPAETGCHFT 182
 182 VGRFTSTHGYEELPLOTFASSGTCGEPISTPLPTVRRVAGRLYSRAIQGVANDEF 241
 183 LSSSTISTHNEEELPMDTFIVSTNPNTVSTTIPGSRPVARGLYSRITQOVKVVDPAP 242
 242 LTRPSSLTVDNPAFE--PVDTTLTFEPRS--NVPSDFMDIIRLHRPALTSRGTRESRL 295
 243 VTTPTKLITVDNPAFEGIDVDNLTFFSSNDNSINADPPFDLIALHRPALTSRGTGIR 302
 296 FSRIGQATMETRSQTQIGARVHFYHNDISPTAPSEYIELQPLVSATEDNGLFDIYADDIDPAM 343
 303 YSRIGKQTLRTSGKSGIGARVHFYHNDISPTAPAE--IELQITPSTVYTTSHASPTSI 361
 344 DNGLFDIYADDI---DPAVVPSPRTTSSAVSYSPTISSASSSVNVTVPVLTSSMDVPVY 400
 362 NNGLYDIYADDITDTSTTPVSPVSTSS--LSGTVP-----ANTTIFEGGAYNTPLV 411
 401 TGPDTLPTSVMPVYSPVTAPOY--IGIHGTHYVLMPLYYFIPKKRRKVPYFEADGEV 459
 412 SGPDIPINITDQAPSLIPVPGSPQYITADAGDFYLPBPTYMLRKRRKRLPYFFSDVSL 471
 460 AA 461
 472 AA 473

```

RESULT 9
AAW03562
ID AAW03562 standard; protein; 601 AA.
XX
AC AAW03562;
XX
DT 22-JAN-1997 (first entry)
XX
DE Human papillomavirus L2E7 fusion protein.
XX
KW HPV; L2 protein; E7 protein; antigen; vaccine; condyloma; wart;
XX
OS Chimeric human papillomavirus type 6;
XX
OS Chimeric synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 596..601
FT /label= Hexa-histidine_tag
XX
PN W09626277-A1.
XX
PD 29-AUG-1996.
XX
PF 23-FEB-1996; 96MO-GB00397.
XX
PR 28-JUL-1995; 95GB-0015478.
PR 24-FEB-1995; 95GB-0003786.
PR 08-JUN-1995; 95US-0000034.
XX
PA (CANTAB) CANTAB PHARM RES LTD.
XX
PI Carmichael JP, Connor SE, Thompson HSG, Whittle NR;
PI Wilson MJ;
XX
DR MPI; 1996-402368/40.
DR N-PSDB; AAT39341.
XX
PT New papilloma virus fusion protein aggregate compns. - comprising
PT the PV L2 and pref. E7 antigens, used in vaccines for prophylaxis or
PT therapy of papilloma virus-associated conditions
XX
PS Disclosure; Fig 1; 45pp; English.
XX
CC An L2E7 fusion protein (AAW03562) comprises a fusion of the L2 and E7
CC proteins of human papillomavirus (HPV). It is encoded by an
CC expression construct (see also AAT39341) obtd. by PCR amplification
CC of HPV-6 viral DNA isolated from a clinical isolate of wart tissue.
CC The fusion protein be expressed in eukaryotic or prokaryotic
CC transformed host cells. Other fusions, comprising L2 or L1 with
CC E1, E2, E4, E5 or E6 proteins from other HPV types, can also be
CC produced. The fusion proteins are useful in vaccines and
CC immunogenic compns.
XX
SO Sequence 601 AA:

Query Match 47.2%; Score 1134; DB 17; Length 601;
Best Local Similarity 50.8%; Pred. No. 1.3e-76;
Matches 236; Conservative 75; Mismatches 136; Indels 18; Gaps 10;

```

```

DB 212 APTTSHPIEIPLDIFVYISSDSGPTSTPVEGTAPR---PRVGLYSRALHQVYTDPA 268
QY 241 FLTRPSSLITYDNPAPFVDTTLTFEPRS--NVPDSDFMDIILHHPALSRGTRFSR 298
DB 269 FLSTPQRLITYDNPVYEGEVSQFSDSIHNNAPDEAFMDIILHHPALSRGTRVYSR 328
QY 299 LQGRATWTRSGTQIGARVHYFDYDISPIAPSPXYIELQPLVSAITEDNGLFDIYADDIPA 358
DB 329 IGRGSMWTRSGKHIGARIHIFYDISPIAQAAEIEHPIVAAQEDT--FDIAKSFEPD 386
QY 359 MPYPSRPTSSANVTSPYISSASS--YSANVTPLTSSWDVYVYTGPDITLPPPTWPIYS 417
DB 387 INPTQHPVYNIISPTVLTSPNVTQPMGNATVPLSIPNDLFLQSGDIDFPPTAPMGTPFS 446
QY 418 PTPAPA-STOYIGIGHYVLYLPIYFIPKRRKRVPEFADGFVAA 461
DB 447 PVPFALPTGPFVFTTSGGFYHPMYAFKRRKRKIDPLFFSD--VAA 489

RESULT 10
AAB23926
ID AAB23926 standard; protein; 473 AA.
XX
AC AAB23926;
XX
DT 18-JAN-2001 (first entry)
XX
DE Human papillomavirus 16 L2 protein SEQ ID NO:2.
XX
KW Human papillomavirus; HPV16; HPV18; L1 protein; L2 protein; antiviral;
KW vaccine; immunisation; immune response; infection; diagnosis.
XX
OS Human papillomavirus.
XX
PN W0200054730-A2.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000MO-US06017.
XX
PR 18-MAR-1999; 99US-0125208.
PR 12-AUG-1999; 99US-0148544.
XX
PA (HARD) HARVARD COLLEGE.
PA (HARR) HARRISON S.
PA (CHEN/) CHEN X.
XX
PI Harrison S, Chen X;
XX
DR WPI; 2000-628165/60.
XX
PT Composition comprising multimer of human papillomavirus L1 protein
PT useful as vaccines against human papillomavirus infection, as
PT diagnostic tools for detecting presence of the virus in biological
PT samples -
XX
PS Disclosure; Page 30; 31pp; English.
XX
CC The present invention describes a composition (I) comprising a multimer
CC of human papillomavirus (HPV) L1 protein (II) which is truncated at its
CC amino terminus. (I) has antiviral activity and can be used in the
CC production of a vaccine. (I) comprising a multimer of HPV L1 protein
CC (a T=1 icosahedral particle comprising a pentamer of L1 protein, one of
CC which comprises HPV L2 protein) when administered induces an immune
CC response against the L1 protein in the humans and is thus useful for
CC immunising the humans against HPV. (I) is thus useful as vaccines against
CC human papillomavirus infection, as diagnostic tools for detecting the
CC presence of HPV in biological samples and as tools for mapping receptor
CC interactions. The present sequence represents an HPV16 L2 protein
CC sequence which is used in the exemplification of the present invention.
XX
SQ Sequence 473 AA:

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CC antigens, which reduces the likelihood of escape mutants, also
 CC immunosuppressive epitopes that may be present in whole antigens can be
 CC avoided with the use of epitope-based vaccines. An additional advantage
 CC is the ability to combine selected epitopes (CTL and HTL) and to modify
 CC the composition of the epitopes achieving enhanced immunogenicity, the
 CC major benefit of the vaccine is that is safe and efficacious. AAB93391
 CC of AAB98477 represent polypeptide sequences used in the exemplification
 CC of the present invention.

XX Sequence 459 AA;

Query Match 47.0%; Score 1130; DB 22; Length 459;
 Best Local Similarity 50.1%; Pred. No. 1.8e-76;

Matches 235; Conservative 77; Mismatches 139; Indels 18; Gaps 10;

QY 1 MSHRAARAKRASYTDLYKTKOSGCPDQVNVKVEGTLADKILQMSLGIPIGLIG 60
 DB 1 MAHSRARRRRKASNTOLYQCKLGTGCPDVIPEVHTINDQILKMSLGVFEGGLIG 60
 QY 61 TGSCTGRTGTYPLGKSNVVDVGP-TRPPVVEVPGETDPSIVTLIEDSSVYTSAPR 119
 DB 61 TGSCTGRTGTYPLGTSKAPSTISGPMARPPVVEVPASDPSIVSLIEESAIINAGAPE 120
 QY 120 PTFGTSGFDITSGTTPAVLDITPSSVSISTNTNFAFSDPSIIEVPQGEVSGN 179
 DB 121 IVPAGHGGFTITSSSETTPALIDVSVTSH--TTSIFRNEVTEPSTVQPPVEANGH 177
 QY 180 VFVGTPTSGHGEIEIPLOTFASGSGEPISTPLP-TVRRVAGPR-LYSRAVOQVSV 236
 DB 178 ILISAPITTSPIEIPDLDFVIVSSDSGPTSTPVPOTAR---PRKGLTSRALHQVQY 234
 QY 237 ANPEFLRPSLLIYDNPAPVDTTLFEPRS--NVPDSFMDIIRLHRPALTSRGTV 294
 DB 235 TDPAFLSTPOLLIYDNPVVEGEVSVQFSHDSIHNAVDEAFMDIIRLHRPALISRGLY 294
 QY - 295 RFSRLGQRATMFTSSGTOIGARVHFYHDISPIASPEYIELOPLVSATEDGLDIYAD 354
 DB 295 RYSIIGRGSMHTSSGKHIGRIHYFDISPIAQAETEMHPLAADDY--FDIVAES 352
 QY 355 IDPAPVPSRPTSSASVTSPTISSASS-YSNVTPLTS-SWDVYVYTGPDITLPTSV 412
 DB 353 FEEDINPTQHVNTISPTYLSTPNTVYQPMGNTTVLSSIPNDLFQSGPDIDIFFPAPM 412
 QY 413 WPIYSPAPASTOYIGIHGTHYLMPLLYFPKRRKRYPPYFADGFAVA 461
 DB 413 GTPSPVYALPTGPFVITGSGFLAPAMYFARKRRKRRIPLFFSD--VAA 459

RESULT 14

AA878317 standard; Protein; 473 AA.

AA878317;

12-MAR-1996 (first entry)

Human papillomavirus 16 wild-type L2 capsid protein.

XX DNA binding activity; human papillomavirus; HPV16; L2 capsid protein;
 KW N-terminal mutation; deletion; substitution; virus-like particle; VLP;
 KM cervical cancer; vaccine.

XX Human papillomavirus 16.

XX Key Location/Qualifiers

FT Misc-difference 50

FT Misc-difference 371 /note= "corresponds to an ACT codon"

FT W09520659-A1.

XX PD 03-AUG-1995.

XX 31-JAN-1995; 95WO-AU00043.
 XX 31-JAN-1994; 94AU-0003588.

XX (CSLC-) CSL LTD.
 XX (UYOU) UNIV QUEENSLAND.

XX Frazer I, Zhou J;

XX WPI, 1995-275444/36.

XX N-PSDB; AA095109.

XX Modified papilloma virus L2 protein - which binds a minimal amt. of
 XX DNA, used for producing virus-like particles for use in vaccines

XX Disclosure: Fig 8; 35pp; English.

CC The N-terminus of HPV16 L2 capsid protein was identified as being
 CC important for DNA binding. Certain mutations (deletions or
 CC substitutions) in the wild-type N-terminal sequence can abolish or
 CC reduce DNA binding. Mutant HPV16 L2 protein which does not bind, or
 CC which binds only a minimal amt. of, DNA will be useful for producing
 CC virus-like particles which only incorporate a minimal amt. of DNA
 CC and are therefore suitable for use in vaccines.
 CC DNA coding for the mutant N-terminal sequences is claimed.

XX Sequence 473 AA;

Query Match 46.9%; Score 1128.5; DB 16; Length 473;
 Best Local Similarity 49.0%; Pred. No. 2.5e-76;

Matches 236; Conservative 74; Mismatches 131; Indels 41; Gaps -12;

QY 6 AARRKASVPTLYTKOSGCPDQVNVKVEGTLADKILQMSLGIPIGLIGTSGT 65
 DB 7 AKRRKRASATOLYTKCKAGTCPPDILPKVAGKTIAEDLIQSGMGVFGGLIGTSGT 66
 QY 66 GGRGTIYPLGGRSNVVD-VGTRPPVVEVPGETDPSIVTLIEDSSVYTSAPR--PTF 122
 DB 67 GGRGTIYPLGRRPTATDTLAPVRPPLVDPVGSIPSVLVEETSRIDAGAPTSVPSI 126
 QY 123 -TGSFPTISAGTTPAVLDITPSSVSISTNTNFAFSDPSIIEVPQGEVSGNF 181
 DB 127 PPDVSGFSITSTDTPTALIDINNVTYV---TTHNNPFTDPSVLPPTPAETGGHFT 182
 QY 182 VGTPTSGHGEIEIPLOTFASGSGEPISTPLP-TVRRVAGPR-LYSRAVOQVADPEF 241
 DB 183 LSSSTISHNKEEIPMDTIFVSTPNVTYTSSTPIGSRPARLGLVSTTQVAVDPPF 242
 QY 242 LTRPSSLITVDNPAFE--PVDITLFEPRS-----VDSDFMDIIRLHRPALTSRGTVR 295
 DB 243 VTPPTKLITVDNPAVEGIDVNTLYFSNDSINIAADPDLVALHAPALTSRRGIR 302
 QY 296 FSRIGQRATMFTSSGTOIGARVHFYHDISPIASPEYIELOPLVSATED----- 343
 DB 303 YSRIGNQOTLRTRGSKSGAKVHYDLSITDPAE-IELOITIPSTYTTTSHAASPTSI 361
 QY 344 DNGLEFDIYADI--DPAMPVPSRPTSSASVTSPTISSASSYSNVTPLTSSWDVYV 400
 DB 362 NNGLYDIYANDFTDTSTTPVPSVTS--LSGITP-----ANTTIPGGKYNPLV 411
 QY 401 TGPDTLPTTSVMPVSPAPASTOY-IGIHGTHYLMPLLYFPKRRKRYPPYFADGFA 459
 DB 412 SGPDIPINTDQASLPIYVGSQYIILADAGFYLHAPSYMKRRKRRIPLFFSDVSL 471
 QY 460 AA 461
 DB 472 AA 473

RESULT 15

AAW44291 standard; Protein; 601 AA.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 17, 2003, 11:02:14 ; Search time 43.3378 Seconds
(without alignments)
1743.646 Million cell updates/sec

Title: US-08-913-644-4

Perfect score: 2405
Sequence: 1 MVSRRARRRRASVTDLTKT.....FIPKRRKRVYFADGFAVA 461Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 609560 seqs, 163917102 residues

Total number of hits satisfying chosen parameters: 609560

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications, AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2317.5	96.4	462	11	US-09-991-053-4
2	2317.5	96.4	462	15	US-10-301-260A-4
3	1133.5	47.1	473	11	US-09-991-053-2
4	1133.5	47.1	473	15	US-10-301-260A-2
5	1131	47.0	459	12	US-10-224-999A-3470
6	667	27.7	519	12	US-10-224-999A-3468
7	639.5	26.6	533	12	US-10-224-999A-3471
8	408.5	17.0	469	12	US-10-305-765-6
9	408.5	17.0	469	12	US-10-305-765-8
10	408.5	17.0	469	12	US-10-305-633-6
11	408.5	17.0	469	12	US-10-305-633-8
12	174.5	7.3	528	12	US-09-840-746-20
13	170.5	7.1	5179	9	US-09-922-217-1068
14	170.5	7.1	5179	10	US-09-833-263-1068
15	170.5	7.1	5179	14	US-10-025-380-1068

16	168	7.0	1367	10	US-09-801-368-108	Sequence 108, App
17	154.5	6.4	1443	15	US-10-245-802-18	Sequence 18, Appl
18	151.5	6.3	605	10	US-09-801-368-428	Sequence 428, App
19	149.5	6.2	314	15	US-10-043-487-311	Sequence 311, App
20	149	6.2	1794	12	US-09-965-738-299	Sequence 299, App
21	149	6.2	1799	12	US-09-965-738-149	Sequence 149, App
22	149	6.2	1821	15	US-09-965-738-82	Sequence 82, Appl
23	149	6.2	5877	15	US-10-142-515-11	Sequence 11, Appl
24	149	6.2	5935	15	US-10-243-243A-8	Sequence 8, Appl
25	149	6.2	11721	12	US-09-965-738-162	Sequence 162, App
26	148	6.2	2971	15	US-10-146-473-50	Sequence 50, Appl
27	145.5	6.0	957	12	US-09-840-746-19	Sequence 19, Appl
28	145.5	6.0	1322	10	US-09-801-368-114	Sequence 114, App
29	144.5	6.0	957	9	US-09-922-217-1065	Sequence 1065, Ap
30	144.5	6.0	957	10	US-09-833-263-1065	Sequence 1065, Ap
31	144.5	6.0	1537	14	US-10-025-380-1065	Sequence 1065, Ap
32	144	6.0	1537	10	US-09-801-368-104	Sequence 104, App
33	141	5.9	1260	15	US-10-245-802-8	Sequence 8, Appl
34	140.5	5.8	688	9	US-09-864-761-36047	Sequence 36047, A
35	140	5.8	2468	12	US-10-246-330-4	Sequence 4, Appl
36	139.5	5.8	878	15	US-10-157-031-171	Sequence 171, App
37	136.5	5.7	1047	15	US-10-245-802-22	Sequence 22, Appl
38	134.5	5.6	1728	12	US-10-032-585-7641	Sequence 7641, Ap
39	131.5	5.5	941	14	US-10-124-557-14	Sequence 14, Appl
40	131.5	5.5	1022	14	US-10-124-557-84	Sequence 84, Appl
41	131.5	5.5	1038	14	US-10-124-557-74	Sequence 74, Appl
42	131.5	5.5	1049	14	US-10-124-557-58	Sequence 58, Appl
43	131.5	5.5	1056	14	US-10-161-510-10	Sequence 10, Appl
44	131.5	5.5	1140	14	US-10-124-557-104	Sequence 104, Appl
45	131.5	5.5	1270	14	US-10-124-557-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-991-053-4
; Sequence 4, Application US/09991053
; Publication No. US20030003532A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen
; TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
; FILE REFERENCE: Harvard/Harrison 12687/1120
; CURRENT APPLICATION NUMBER: US/09/991,053
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-18
; PRIOR APPLICATION NUMBER: 60/125208
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/148544
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-09-991-053-4

Query Match 96.4%; Score 2317.5; DB 11; Length 462;
Best local Similarity 96.8%; Pred. No. 4.2e-182;
Matches 447; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 MVSRRARRRRASVTDLTKRKSGGTCPSVYVKKVEGTITADKIIQWSSIGITLGLGIG 60
DB 1 MVSRRARRRRASVTDLTKRKSGGTCPSVYVKKVEGTITADKIIQWSSIGITLGLGIG 60
QY TSGGTGRCGYITLGGRSNTVVDGPTRPVVIIEPGTDPSTIVTLIEDSVYTSAPRP 120
DB 61 TSGGTGRCGYITLGGRSNTVVDGPTRPVVIIEPGTDPSTIVTLIEDSVYTSAPRP 120

[illegible]

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RESULT 2
US-10-301-260A-4
; Sequence 4, Application US/10301260A
; Publication No. US20030118609A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen
; APPLICANT: Chen, Xiaojiang
; TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
; FILE OF INVENTION: virus
; FILE REFERENCE: Harvard/Harrison 12687/1123
; CURRENT APPLICATION NUMBER: US/10/301,260A
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 09/520, 822
; PRIOR FILING DATE: 2000-03-18
; PRIOR APPLICATION NUMBER: 60/125208
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/148544
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 462
; TYPE: PRF
; ORGANISM: Human papillomavirus type 18
; US-10-301-260A-4

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Query Match	96.4%	Score 2317.5	DB 15	Length 462
Best Local Similarity	96.8%	Pred. No. 4.2e-182		
Matches 447	Conservative 5	Mismatches 9	Indels 1	Gaps 14

QY 1 MVSRRARRRRKAASTVDLTKFTCKOSGTCSDVNNVEGTTLADKILQWSLSIFLGGGLG 60
1 MVSRRARRRRKAASTVDLTKFTCKOSGTCSDVNNVEGTTLADKILQWSLSIFLGGGLG 60
Db 1 MVSRRARRRRKAASTVDLTKFTCKOSGTCSDVNNVEGTTLADKILQWSLSIFLGGGLG 60
QY 61 TGSGTCGRCTGIFLGGRSNTVYDVGPRRPVYIEVGTPDTSIYTLIEDSSVYTSGARPR 120
61 TGSGTCGRCTGIFLGGRSNTVYDVGPRRPVYIEVGTPDTSIYTLIEDSSVYTSGARPR 120
Db 61 TGSGTCGRCTGIFLGGRSNTVYDVGPRRPVYIEVGTPDTSIYTLIEDSSVYTSGARPR 120
QY 121 TFGTSGCFDITSACTTTPAVLDLNPSSSTSVSISTTNFNPAFSDPSIIIEVPQTGEVGNV 180
121 TFGTSGCFDITSACTTTPAVLDLNPSSSTSVSISTTNFNPAFSDPSIIIEVPQTGEVGNV 180
Db 121 TFGTSGCFDITSACTTTPAVLDLNPSSSTSVSISTTNFNPAFSDPSIIIEVPQTGEVGNV 180
QY 181 FVCGPTGCTGGEYIEIPLQTFASSSGTGEERISSTPLPYRRVAGCPLYSRAAOVSVAPAE 240
181 FVCGPTGCTGGEYIEIPLQTFASSSGTGEERISSTPLPYRRVAGCPLYSRAAOVSVAPAE 240
Db 181 FVCGPTGCTGGEYIEIPLQTFASSSGTGEERISSTPLPYRRVAGCPLYSRAAOVSVAPAE 240
QY 241 FLRRPSLLIYDNPAPFVDTTLTFEERSNVPDSDMDIILRLHAPALTSRRGVAFNRIG 300
241 FLRRPSLLIYDNPAPFVDTTLTFEERSNVPDSDMDIILRLHAPALTSRRGVAFNRIG 300

Db	241	FLRPSLLITTYDNPAPPEPVDITLTLPDSVDYDDSDFMDIILRLHAPALTSRRGTVRRSRLG	300
Oy	301	QRAATMTBRSQTQGAARVHFHDISPIASPEYIELQPLVSTEDNGLFYIADIDPAMP	360
Db	301	QRAATMTBRSQTQGAARVHFHDISPIASPEYIELQPLVSTEDNDFDIADMDMPAVP	360
Oy	361	VPAPPTSSAVSTSPSTISSASSYNNVPLTSSMDVYVYVGGDITLP-PLSWPPIVSPR	419
Db	361	VPAPSTTSRPFERISPTTSSASSYNNVPLTSSMDVYVYVGGDITLPSTTSWPIVSPR	420
Oy	420	APASTQYIGIGHYHLYMLPYFIPIPKRRKRVYFFADGEVAA	461
Db	421	APASTQYIGIGHYHLYMLPYFIPIPKRRKRVYFFADGEVAA	462

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RESULT 3
US-09-991-053-2
; Sequence 2, Application US/09991053
; Publication No. US2003000352A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen
; APPLICANT: Chen, Xiaojiang
; TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
; FILE OF INVENTION: virus
; FILE REFERENCE: Hayward/Harrison 12687/1120
; CURRENT APPLICATION NUMBER: US/09/991,053
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-18
; PRIOR APPLICATION NUMBER: 60/125208
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/148544
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 473
; TYPE: PR1
; ORGANISM: Human papillomavirus type 16
US-09-991-053-2

```

Query Match	47.1%	Score 1133.5	DB 11	Length 473
Best Local Similarity	49.2%	Pred. No. 8.6e-85		
Matches 237	Conservative 73	Mismatches 131	Indels 41	Gaps 12

```

QY 6 AARAKSAVTDJLKKFKCQSGCPCSPVKNKVGCTLLAKLLOMSLGFGLGGLGNGSGT 65
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 AKRTKASATOLTKTKCQAGTCPPDILIKVAGKTIAGDILLOQSGMVGFFGGLGIGSGT 66
QY 66 GGRGTGYPILGKRSNTVVD-VGPTRPVYIEVGPITDSIVTLIEDSSVYVSGAPR--PTF 122
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 GGRGTGYPILGTRPATDILAPVRPLVHDVGPDSISVLEETSFIDAGAPTSVPSI 126
QY 123 -TGTSEFDITSAAGTTTPAVLDTIBSTSVSLSTINFTNPAFSDPSLIEVQIGSVGNVF 181
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 PPDVSESTSTSTSTDTTPALDILINNTVTV---LTTHNNPTFTPSVLQPTPARETGHEFT 182
QY 182 VGPPTSGTGHGEIPILOTFASAGTGEPIISSTPLTVRAVAGPLTSRAQOVSVANPEF 241
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 183 LSSSTISHNHYEIMDFIYSTINNTVYSTPTFGSRPARAGLISRTTQOVKVVDPAF 242
QY 242 LRRPSSLITYVDPAFE--PVDITLFEERSN---VPDSDFMDIRLHRPALYSRGTVR 295
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 VTTPTFKLTYDPAVEGIDVDNTLYFSSNDNSINIAVDPDFLDIYALHRLPALYSRTGIR 302
QY 296 FSRLOKATMTFRSGTOIGARVHYHIDISPLASPEVIELOPLVSATE----- 343
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 303 YSRIGKOTLRTSRGSKIGARVHYHYDLSITDPAEE-IELOTPSTVYTTSHAASPTSI 361
QY 344 DNGLEFDIYADCI---DPAMPVSRPSTSAVSTSPSISSASSYVNTVPLDSMWQVYX 400
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 362 NNGLDIYADDIYDSTTTPVSPVSPS--LSGITP-----ANTLTPPGGAVNIPLY 411

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QY 401 TGPDIILPPTSWPIYSPAPASTQY-IGIHGHYIYMLPLYIPKRRKRVPEFADGV 459
 Db 412 SGPDILPINITDQAPSLPIVPGSPQYTIADAGDFYLBHSYMLRKRKRRLPYFSDVSL 471
 QY 460 AA 461
 Db 472 AA 473

RESULT 4

US-10-301-260A-2
 ; Sequence 2, Application US/10301260A
 ; Publication No. US20030118609A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harrison, Stephen
 ; APPLICANT: Chen, Xiaojiang
 ; TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
 ; TITLE OF INVENTION: virus
 ; FILE REFERENCE: Harvard/Harrison 12687/1123
 ; CURRENT APPLICATION NUMBER: US/10301, 260A
 ; PRIOR FILING DATE: 2002-11-21
 ; PRIOR APPLICATION NUMBER: 09/520, 822
 ; PRIOR FILING DATE: 2000-03-18
 ; PRIOR APPLICATION NUMBER: 60/125208
 ; PRIOR FILING DATE: 1999-03-18
 ; PRIOR APPLICATION NUMBER: 60/148544
 ; PRIOR FILING DATE: 1999-08-12
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID-NO 2
 ; LENGTH: 473
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 ; US-10-301-260A-2

Query Match 47.1%; Score 1133.5; DB 15; Length 473;
 Best Local Similarity 49.2%; Pred. No. 8.8e-85;

Matches 237; Conservative 73; Mismatches 131; Indels 41; Gaps 12;

QY 6 AARRKASVYDLYKTKQSGTCPSDVNVKVEGTTLADKILQMSLIGIFLGIGTSGT 65
 Db 7 AKRTKASATQLYKTKQSGTCPSDVNVKVEGTTLADKILQMSLIGIFLGIGTSGT 66
 QY 66 GGTGTGTPGAGSNVYD-VGPRPVVIEPVGTPDSTVLTLEDSVVTGAPR-PTF 122
 Db 67 GGTGTGTPGAGSNVYD-VGPRPVVIEPVGTPDSTVLTLEDSVVTGAPR-PTF 126
 QY 123 -TGTSGFDITSAGTTTAVLDITPSTSVSISTNTNTPAFSDPSIIEVQTGEVGNV 181
 Db 127 PPVSEFSITSTDTTALDINNVTYV---TTHNNPTFTDPSVLDQPTPAETGGHT 182
 QY 182 VGTPTSGTGEYERIPLOTFASGSGTGEPISTPLPTVRVYAGPLXSRAYQVSVANPEF 241
 Db 183 LSSSTISTHNEYEIPMDTFIVSNPMTVTSSTPIPSRPVARGLVSRTQYKVVDPAF 242
 QY 242 LTPSSLIYDNPAAE--PYDTLTLEPRSN---VPDSDFMDIIRLHRPALTSRGTVR 295
 Db 243 VTPPTLIYDNPAYEGIDVNTLFFSSNDNSINIAIPDPLDIVALLHRPALTSRGTGIR 302
 QY 296 FSRLOGRATMTFSSGOIGARVHYDISPIASPEYIELOPLVSATE----- 343
 Db 303 YSRIGNKQTLRTSSGKIGAKVHYDLSIDPAEE-IELOTTPTSTYTTSSHAASPTSI 361
 QY 344 DNGLFYIYADDI---DPAMPVSRPTSSAVSTYPTISSASSVNTVPLTSSMDPVY 400
 Db 362 NMLYIYIYADDITDSTTPVPSVPTS--LSGTIP-----ANTTIFGAGYINPLV 411
 QY 401 TGPDIILPPTSWPIYSPAPASTQY-IGIHGHYIYMLPLYIPKRRKRVPEFADGV 459
 Db 412 SGPDILPINITDQAPSLPIVPGSPQYTIADAGDFYLBHSYMLRKRKRRLPYFSDVSL 471
 QY 460 AA 461
 Db 472 AA 473

Db 472 AA 473

RESULT 5

US-10-224-999A-3470
 ; Sequence 3470, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavit, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224, 999A
 ; CURRENT FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313, 695
 ; PRIOR FILING DATE: 2001-08-20
 ; NUMBER OF SEQ ID NOS: 3484
 ; SOFTWARE: Patentln version 3.1
 ; SEQ ID NO 3470
 ; LENGTH: 459
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 6b
 ; US-10-224-999A-3470

Query Match 47.0%; Score 1131; DB 12; Length 459;
 Best Local Similarity 50.1%; Pred. No. 1.3e-84;

Matches 235; Conservative 77; Mismatches 139; Indels 18; Gaps 10;

QY 1 MSHRAARRKASVYDLYKTKQSGTCPSDVNVKVEGTTLADKILQMSLIGIFLGIGT 60
 Db 1 MAHSRAARRKASVYDLYKTKQSGTCPSDVNVKVEGTTLADKILQMSLIGIFLGIGT 60
 QY 61 TSGGTGRTGYIPLGGSNTVYDGP--TRPVVIEPVGTPDSTVLTLEDSVVTGAPR 119
 Db 61 TSGGTGRTGYIPLGGSNTVYDGP--TRPVVIEPVGTPDSTVLTLEDSVVTGAPR 120
 QY 120 PPTGTSGFDITSAGTTTAVLDITPSTSVSISTNTNTPAFSDPSIIEVQTGEVGN 179
 Db 121 TVPAGGFGTITSETTPTALIDVSVTSH---TTSIFRNPVTEBESVNGPOPVEANGH 177
 QY 180 VFTGTPTSGHGEYERIPLOTFASGSGTGEPISTPLPTVRVYAGPLXSRAYQVSV 236
 Db 178 ILISAPLVYSHPEEIPLDTFVYSSDSGPTSTPVGTAPR---PRVGLYSRALQVY 234
 QY 237 ANPEFLRPSLSLTYDNPAPVDTLTLEPRR--NPDSDFMDIIRLHRPALTSRGTV 294
 Db 235 TDPALFSTPRLITTDNPVTEGEDVSVOFSDSHINAPDAFMDIIRLHRPALTSRGLV 294
 QY 295 RFSRLGQRATMTFSSGOIGARVHYDISPIASPEYIELOPLVSATEDNGLEFDIYAD 354
 Db 295 RYSGIRGSGMHRSGKHIGARHYFIDISPIAQAABEIMHPLVAAQDDT--FDIYAES 352
 QY 355 IDPAMPVSRPTSSAVSTYPTISSASS--YSNVTVPLTSSMDPVYTGDIILPPTSW 413
 Db 353 FEEGINTQHPVYNISDPTVLTSTPNVTQPGWTVYPLSLPNDLFLQSGPDIFPPAPMG 412
 QY 414 PIVSPAPAA-STQYIGIHGHYIYMLPLYIPKRRKRVPEFADGVAA 461
 Db 413 TPFSVTPALPTGPFVITGSGFYIHPAMYFARRKRRIPLFSD--VAA 459

RESULT 6

US-10-224-999A-3468
 ; Sequence 3468, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavit, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection


```

; TYPE: PR
; ORGANISM: Bovine papillomavirus type 1
; FEATURE:
; OTHER INFORMATION: L2 open reading frame (wild-type)
US-10-305-765-6

```

```

Query Match      17.0%; Score 408.5; DB 12; Length 469;
Best Local Similarity 29.3%; Pred. No. 3.3e-25;
Matches 152; Conservative 59; Mismatches 174; Indels 133; Gaps 24;

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```

QY 8 RRRASVVDLYKTKOSGTCPSDVVNVKVGTTLADKILLOMSIGIFLGIGTGS----- 63
DB 6 RKRASADLYKTKOAGTCPPDVIRKVGDTIADILKFGGLATILGGLGIGTGSTGV 65
QY 64 GTGRTGYIPL--GGRSNTVVDGP-----TRPV-----VIEPVGTPDSI--VT 105
DB 66 AAGGSPRYTPLRTAGSTSSLASIGSRAYTAGTSPISGAGIPLDTLETGLALRGVYEDIV 125
QY 106 LIEDSSVYVTSGARPTFTGSGFDITSAGTTP-----AVIDTP--SST 148
DB 126 LPEAPALVTPDA---VPADSGIDLSTGDSSTETLITLLEPEGPEDIAYVLELOLDRP 181
QY 149 SVSISTNTNTPAFSDPSIIEVPTGEVSG--NVEVGTPTSGHGEELPLQTFASGSG 206
DB 182 TWQVSNAYVQSSAYVAPLQLO--SIAETSGLENIIFVGGGLDGTGENIELTYFGS---- 236
QY 207 EEPISSTPLPYRVAVGPRLY--SRAYQVSVANPEFLTRPSSLITYDNPAEPVDTTLT 264
DB 237 --PRISTSPRIASKRGILNMFSCRYYTQVPEDEPVF-----SSQTFANPLVEA----- 284
QY 265 PEPRSNVPSDPMIIRLRPALTSRGTGVRSRGQRATMTTRSGTOIGANVHEHYHDS 324
DB 285 --EP-----AVLKGPSGRVGLSQVKKPDTLTRSGTEVGPQLHVAYSLIS 326
QY 325 PIAPSEYI-----ELOPLVSATEDNGLEFIYADDIDPA--NP----- 360
DB 327 THEDEVALPYVDENTOGIAFVPL--HEQAGFEEIEDDSETHRLILPONTSSPVGS 384
QY 361 -----VPSR---PTTSSAVSTY--SPTISSASSYSNVTVPLTSSMDVPYVGTDTLPT 410
DB 385 GVARSLIPIREFSATRPVTGVVYGGSPDTYSAS-----PVMD---PDSTSPSLVIDT 433
QY 411 SWMPIVSPAPASTGYIGHGHYILMPLYIFPKRK 448
DB 434 TTPPIIIT---IDGHTVDLYSSNYTLHPSLLRKRRK 467

```

```

RESULT 9
US-10-305-765-8
; Sequence 8, Application US/10305765
; Publication No. US20030175907A1
; GENERAL INFORMATION:
; APPLICANT: FRAZER, Ian Hector
; APPLICANT: ZHOU, Jian
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AND METHOD FOR SELECTIVELY
; TITLE OF INVENTION: EXPRESSING A PROTEIN IN A TARGET CELL OR TISSUE
; FILE REFERENCE: 210338.0001/105
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US/10/305,765
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: PCT/AU98/00530
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: AU P07765
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: AU P09467
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 469
; TYPE: PR
; ORGANISM: Artificial Sequence

```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bovine
; OTHER INFORMATION: Papillomavirus type 1 L2 open reading frame
; OTHER INFORMATION: (humanized)
; FEATURE:
; OTHER INFORMATION: Wild-type codons replaced with synonymous codons
; OTHER INFORMATION: used at relatively high frequency by human genes
US-10-305-765-8

```

```

Query Match      17.0%; Score 408.5; DB 12; Length 469;
Best Local Similarity 29.3%; Pred. No. 3.3e-25;
Matches 152; Conservative 59; Mismatches 174; Indels 133; Gaps 24;

```

```

QY 8 RRRASVVDLYKTKOSGTCPSDVVNVKVGTTLADKILLOMSIGIFLGIGTGS----- 63
DB 6 RKRASADLYKTKOAGTCPPDVIRKVGDTIADILKFGGLATILGGLGIGTGSTGV 65
QY 64 GTGRTGYIPL--GGRSNTVVDGP-----TRPV-----VIEPVGTPDSI--VT 105
DB 66 AAGGSPRYTPLRTAGSTSSLASIGSRAYTAGTSPISGAGIPLDTLETGLALRGVYEDIV 125
QY 106 LIEDSSVYVTSGARPTFTGSGFDITSAGTTP-----AVIDTP--SST 148
DB 126 LPEAPALVTPDA---VPADSGIDLSTGDSSTETLITLLEPEGPEDIAYVLELOLDRP 181
QY 149 SVSISTNTNTPAFSDPSIIEVPTGEVSG--NVEVGTPTSGHGEELPLQTFASGSG 206
DB 182 TWQVSNAYVQSSAYVAPLQLO--SIAETSGLENIIFVGGGLDGTGENIELTYFGS---- 236
QY 207 EEPISSTPLPYRVAVGPRLY--SRAYQVSVANPEFLTRPSSLITYDNPAEPVDTTLT 264
DB 237 --PRISTSPRIASKRGILNMFSCRYYTQVPEDEPVF-----SSQTFANPLVEA----- 284
QY 265 PEPRSNVPSDPMIIRLRPALTSRGTGVRSRGQRATMTTRSGTOIGANVHEHYHDS 324
DB 285 --EP-----AVLKGPSGRVGLSQVKKPDTLTRSGTEVGPQLHVAYSLIS 326
QY 325 PIAPSEYI-----ELOPLVSATEDNGLEFIYADDIDPA--NP----- 360
DB 327 THEDEVALPYVDENTOGIAFVPL--HEQAGFEEIEDDSETHRLILPONTSSPVGS 384
QY 361 -----VPSR---PTTSSAVSTY--SPTISSASSYSNVTVPLTSSMDVPYVGTDTLPT 410
DB 385 GVARSLIPIREFSATRPVTGVVYGGSPDTYSAS-----PVMD---PDSTSPSLVIDT 433
QY 411 SWMPIVSPAPASTGYIGHGHYILMPLYIFPKRK 448
DB 434 TTPPIIIT---IDGHTVDLYSSNYTLHPSLLRKRRK 467

```

```

RESULT 10
US-10-305-633-6
; Sequence 6, Application US/10305633
; Publication No. US20030182674A1
; GENERAL INFORMATION:
; APPLICANT: FRAZER, Ian Hector
; APPLICANT: ZHOU, Jian
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AND METHOD FOR SELECTIVELY
; TITLE OF INVENTION: EXPRESSING A PROTEIN IN A TARGET CELL OR TISSUE
; FILE REFERENCE: 210338.0001/105
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US/09/479,645
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: PCT/AU98/00530
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: AU P07765
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: AU P09467
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6

```

```
;; LENGTH: 469
;; TYPE: PRT
;; ORGANISM: Bovine papillomavirus type 1
;; FEATURE:
;; OTHER INFORMATION: L2 open reading frame (wild-type)
US-10-305-633-6

Query Match      17.0% Score 408.5; DB 12; Length 469;
Best Local Similarity 29.3%; Pred. No. 3.3e-25;
Matches 152; Conservative 59; Mismatches 174; Indels 133; Gaps 24;

      8 RRRKASVTDLYKTCQSGTCDPSDVNVEGTTLADKILWSSLSGIFLGIGTGS----63
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6 RKRASAYDLKRTCKQKAGTCDPPDIRKVEGDTLADKILKGLAIVYGGIGTWSGTV 65
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 64 GTGRTGYIDL--GGRSNVVDVGP-----TRPPV-----VIEPVGPTDSI---VT 105
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 AAGSPRYTLRTAGSTSSLASIGRAVTAAGRPSIGAGIPDLTLFTLGLALRPGVEDTV 125
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 106 LIEDSVVTSGAPRPTGTSGFDITSAQTTP-----AVLDTTP--SST 148
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 LPEAPALVTPDA---VPADSGLDALSTIGDSTETTLTLEPBGPDIAVLELQPLDRP 181
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 149 SVSISTNTNTPAFSDPSIIEVPQTGEVSG--NVFVGTPSGTHGEEIPLQTFASSGTG 206
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 TMOYSNVAHQSAAHAPLQLO--SIAETSGLENIFVGSGIGDGTGGENIELTYFGS----236
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 207 EEPISSTPLPTVRVAVGRPLY--SRAYQOVSANPEELTRPSLITYDNPAFEPVDTTLT 264
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 237 --PRTSPRISJASRGLMFMFSKRYTQVPTEDPEVF---SSQTFANPLYE-----284
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 265 FEPRSNVPDSDFMIIRLHAPALTSRGTVAFSLGQATMFTSGQIGARVIFYDIS 324
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 285 -EP-----AVLKGPSGRGVLGQVYRPDLTTRSGTEVGPQLHVRYSLS 326
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 325 PIAPSPXYI-----ELOPLVATEDBNGLFDIYADDIDPA---MP-----360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 327 TIHEDVAIPYVDENTOGIAFVPL--HEBOAGFEELDFDSETHRLLPONTSSPTVGS 384
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 -----VPSR---PTSSASVSTY-SPTISSASSYSNTVPLTSSMDVPVYTGPDITLPT 410
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 385 GVRSLIPTREFSATRPGLVTVGSPDTYSAS-----PVTD---PDSTSPSLVIDDT 433
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 411 SVMPIVSPAPASTQYIGIHGTHYLLPPLYFYFIPKRR 448
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 434 TTPIIT-----IDGHTVDLYSSNTTLAPSLLRKRRKK 467
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-10-305-633-8
; Sequence 8, Application US/10305633
; Publication No. US20030182674A1
; GENERAL INFORMATION:
; APPLICANT: FRAZER, Ian Hector
; APPLICANT: ZHOU, Jian
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AND METHOD FOR SELECTIVELY
; FILE REFERENCE: 210338.0001/105
; CURRENT APPLICATION NUMBER: US/10/305,633
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US/09/479,645
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: PCT/AU98/00530
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: AU P07765
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: AU P09467
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 469
; TYPE: PRT
```

```
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Bovine
;; OTHER INFORMATION: papillomavirus type 1 L2 open reading frame
;; FEATURE:
;; OTHER INFORMATION: (humanized)
;; OTHER INFORMATION: wild-type codons replaced with synonymous codons
;; OTHER INFORMATION: used at relatively high frequency by human genes
US-10-305-633-8

Query Match      17.0% Score 408.5; DB 12; Length 469;
Best Local Similarity 29.3%; Pred. No. 3.3e-25;
Matches 152; Conservative 59; Mismatches 174; Indels 133; Gaps 24;

      8 RRRKASVTDLYKTCQSGTCDPSDVNVEGTTLADKILWSSLSGIFLGIGTGS----63
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6 RKRASAYDLKRTCKQKAGTCDPPDIRKVEGDTLADKILKGLAIVYGGIGTWSGTV 65
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 64 GTGRTGYIDL--GGRSNVVDVGP-----TRPPV-----VIEPVGPTDSI---VT 105
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 AAGSPRYTLRTAGSTSSLASIGRAVTAAGRPSIGAGIPDLTLFTLGLALRPGVEDTV 125
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 106 LIEDSVVTSGAPRPTGTSGFDITSAQTTP-----AVLDTTP--SST 148
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 LPEAPALVTPDA---VPADSGLDALSTIGDSTETTLTLEPBGPDIAVLELQPLDRP 181
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 149 SVSISTNTNTPAFSDPSIIEVPQTGEVSG--NVFVGTPSGTHGEEIPLQTFASSGTG 206
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 TMOYSNVAHQSAAHAPLQLO--SIAETSGLENIFVGSGIGDGTGGENIELTYFGS----236
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 207 EEPISSTPLPTVRVAVGRPLY--SRAYQOVSANPEELTRPSLITYDNPAFEPVDTTLT 264
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 237 --PRTSPRISJASRGLMFMFSKRYTQVPTEDPEVF---SSQTFANPLYE-----284
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 265 FEPRSNVPDSDFMIIRLHAPALTSRGTVAFSLGQATMFTSGQIGARVIFYDIS 324
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 285 -EP-----AVLKGPSGRGVLGQVYRPDLTTRSGTEVGPQLHVRYSLS 326
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 325 PIAPSPXYI-----ELOPLVATEDBNGLFDIYADDIDPA---MP-----360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 327 TIHEDVAIPYVDENTOGIAFVPL--HEBOAGFEELDFDSETHRLLPONTSSPTVGS 384
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 -----VPSR---PTSSASVSTY-SPTISSASSYSNTVPLTSSMDVPVYTGPDITLPT 410
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 385 GVRSLIPTREFSATRPGLVTVGSPDTYSAS-----PVTD---PDSTSPSLVIDDT 433
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 411 SVMPIVSPAPASTQYIGIHGTHYLLPPLYFYFIPKRR 448
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 434 TTPIIT-----IDGHTVDLYSSNTTLAPSLLRKRRKK 467
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-09-840-746-20
; Sequence 20, Application US/09840746
; Publication No. US20030166501A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hwei-Mei
; APPLICANT: Honcheil, Cynthia D.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Mucin-Related Tumor Marker
; FILE REFERENCE: PC-0039 US
; CURRENT APPLICATION NUMBER: US/09/840,746
; PRIOR FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Genbank ID No. US20030166501A1 g915208
US-09-840-746-20
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Query Match	7.3%	Score 174.5	DB 12	Length 528
Match Local Similarity	22.1%	Pred. No. 6,7e-06		
Matches 83	Conservative 57	Mismatches 147	Indels 89	Gaps 13
QY	86	PTRPVVVLEPVGPTPSIVTLI-----EDSSVYVSGAPRPFTSGSDIRS	132	
Db	141	PTTSATSVQSSSSSPPISSITVSVQPPSSSSAPTTSSATSVQSSSSSPPISSITVSVQSS	200	
QY	133	AGTT-TPAVLDITPSTSVSISTTNFTNPASDPSITIEVPQGEVGNVFGTPTSGTHG	191	
Db	201	SSSVPTTSTTVQPPSSSS-SVPTTSATSVRSSSSSTPTPTSTTVQPPSSSSAPT-----	254	
QY	192	YEEIPIQTFASSGTFEEP--ISSTPLPTVRRY-----AGPRTYRAYQVAVANDEFLT	243	
Db	255	-----TSATSVQPPSSSSSTPTPTSTTVQPPSSSSAPTTSATSVQPPSSSSP-----	300	
QY	244	RPSLLITYDNPAFEVDDTLTFEPRSNVDDSDFMDIIRLHRPALTSRRCQTVFRSRLGORA	303	
Db	301	-----PISSITTSVQPPSS-----SSSPTTSTTVQPPSSSSGAP	333	
QY	304	TM-----PTRSGQIGARVHFYHDISPIAPSPETIELOPLVSATNEDMGGLDIYADDID	356	
Db	334	TTSATSVQPPSSSSSPPISSITTSVQPPSSSSSTPTTSTTVQPPSSSSGAP---TSATSVQ	389	
QY	357	PAMPVPSRPT-----SSAVSTYSPTTSSASYSNTVPLTSSMDVPPVYTGPDITLP	408	
Db	390	PSSS-SVPTTTSATSVRSSSSSPDIPPTTSVQPPSSSSSVPTTSATSVQTTSSSSSTPTPS	448	
QY	409	PTSVWPIYSPITAPAST	424	
Db	449	TTTSVQPPSSSSSAPPTS	464	

```

RESULT 13
US-09-922-217-1068
: Sequence 1068, Application US/09922217
: Patent No. US20020076414A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Lodes, Michael J.
: APPLICANT: Secretist, Heather
: APPLICANT: Benson, Darin R.
: APPLICANT: Meagher, Madeleine Joy
: APPLICANT: Stolk, John A.
: APPLICANT: Wang, Tongtong
: APPLICANT: Jiang, Yugu
: APPLICANT: Smith, Carole Lynn
: APPLICANT: King, Gordon E.
: APPLICANT: Wang, Aijun
: APPLICANT: Clapper, Jonathan D.
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
: FILE REFERENCE: 210121.471C13
: CURRENT APPLICATION NUMBER: US/09/922,217
: CURRENT FILING DATE: 2001-08-03
: NUMBER OF SEQ ID NOS: 1124
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1068
: LENGTH: 5179
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-922-217-1068

```

Query Match	7.1%	Score 170.5	DB 9	Length 5179
Best Local Similarity	24.3%	Pred. No. 0.00034		
Matches 108; Conservative	42;	Mismatches 163;	Indels 132;	Gaps 23
QY	61	TGSGTGGATGCTGTCPLGGRSNTYVDGQTPRPVYIEVCGPDSIVTLIEDSSVYTGAPRP	120	
Db	3960	TPPLPGTGTGTTTPTTPTTTPVTPPLPCTGTGTPPTTPTTTPPTTTPVTPPP	4021	
QY	121	TFTGTGTTSGFDITSAGITTPAVLDITTTBSSIVSISITNTFTNPAPSPDSIIIEVPQTG	174	

```

Db      4028  TPTGQPTPTTPIITTTTIVTPPTPTGQPTTPIITTTTIVTPPT---PTGQPTPTT 4084
QY      175  EVSGNVEYGPPT---SGTHGYEELPLOTFA-----SGTGEPISSPPLTVRRVAGRL 226
Db      4085  PTTTTTIV-PTPTPTGQPTTPTTPIITTTTIVTPPTPTGQPTTPIITTTTIVT--- 4139
QY      227  YSRVYQGVANPEFLPSSLIT-YONPAPEVDITTEPRSNVPSDMDIIRLHRP 285
Db      4140  -----PTPTPTGQPTTPTTPIITTTTIVTPPT-----P 4167
QY      286  ALTSRGTVFNRSLGQRATMTFSGTOIGARVHFYHDISPIA-----PSDEYIELQ-- 336
Db      4168  TGTQPTPTTPTTTTPTTPTPTGTCGPETH--TSPAPLAEITLTSNPRESSPTQSR 4225
QY      337  ---PLVSATDDNGLFIDYADIDIPAMVY-----PSRTTSSAVSTSP----- 377
Db      4226  STSPLBEST-----TLSTLPALAEIMSTAPSPSTPAATTTTSGHTLSPPSSTTSP 4278
QY      378  -----ISSASSYSNVTPLPSTSM---DYVYVYTGPDITLPTPSVMPVIVSPT--- 419
Db      4279  PGTPTRGTTGSSSAPPSVQTGTTTTSAMTPTPLPLST-PSI-IRTTGLRYPYPSVLIC 4336
QY      420  -----APASTGYIGING-THYYL 436
Db      4337  VLNDTYIAPGEEVINGTGTCTYTP 4361

```

```

RESULT 14
US-09-833-263-1068
; Sequence 1068, Application US//09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833, 263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1068
; LENGTH: 5179
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-833-263-1068

```

Query Match	7.1%	Score 170.51	DB 10	Length 5179
Best Local Similarity	24.3%	Pred. No. 0.00034		
Matches	108	Conservative	42	Mismatches 163; Indels 132; Gaps 23;
QY	61	TGSGTGKRTGILPLGKSNIVYVGGPRRPVIVIEGCTPDSIYTLIEDSSVTVSGAPR	120	
DB	3960	TPRPPIGQYQ---PTTPPIPTTTTTVTPRPPIGQYQ---PTTPPIPT-----TTTTVTPR	4027	
QY	121	TFPGT---SGFDITSAGTTTPAVLDI---TPSSVSISISTNTFNPAISDPSILEVPQTG	174	
DB	4028	TPIGQRPPTTPIPTTTTIVTPRPPIGQYPTTPIPTTTTIVTPRP---PTGQYPTTT	4084	
QY	175	EVSQNVFYGPTT---SGTHGYEELPLOTFA---SGTGEPISSPTPLPVRVAGBRL	226	
DB	4085	PIPTTTTTV-TPRPPIGQYPTTPIPTTTTIVTPRPPIGQYPTTPIPTTTTTVT	4139	
QY	227	YSRAVQVSVANPELFPSSSLIT-YDPAPEPDTITFEPRSNVPSDPMIILHRP	285	
DB	4140	-----PPTPIPGQYPTTPIPTTTTIVTPRP-----P	4167	
QY	286	ALTSRGTVRSRLGORATMTNSGTOIGANVHFYHDISPIA-----PSEVEYELQ--	336	
DB	4168	TGTPQPTTPIPTTTTIVTPRPPIGQYGPPIH---TSPAPLAEITLTPSPRESSPTQSR	4225	

[illegible]

```

RESULT 15
US-10-025-380-1068
: Sequence 1068, Application US/10025380
: Publication No. US20020182191A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Lodes, Michel J.
APPLICANT: Secretist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Mesgher, Madeleine Joy
APPLICANT: Stoik, John A.
APPLICANT: Wang, Tonglong
APPLICANT: Jiang, Yugu
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasar A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025.380
CURRENT FILING DATE: 2001-12-19
NUMBER-OF SEQ ID NOS: 1129
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 1068
: LENGTH: 5179
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-025-380-1068

```

Query Match	7.18;	Score 170.5;	DB 14;	Length 5179;
Best Local Similarity	24.38;	Pred. No. 0.00034;		
Matches 108; Conservative	42;	Mismatches 163;	Indels 132;	Gaps 23;

QY	61	TGSGTGRGTGCTPLPGSRNIVVDGPPRPVIEVGPTDTSIVLIEDSSVTSGAPR	120
Db	3980	TPRPTGQT---PTTTPITTTTTVTPRPRTGQT-PTTTPITTT-----TTTVTPR	4022
QY	121	TFETG---SGCDITSAGTTTPAVLDI---TPSSISVLSITTFNTPAFSDSLIEVPTG	174
Db	4028	TPRTGQTPPTTPTTTTTTTPPTPTPTGQTPTTPTTTTTTTPPT---PTGQTPTTT	4084
QY	175	EVSGNVAVGPT---SGTHGEELPLQFAS---SGTGEPISTPLPRVARVAGPL	226
Db	4085	PITTTTTV-TPRTPTGQTPTTPTTTTTTTPRPRTGQTPTTPTTTTTT	4133
QY	227	YSRAVQOVSANPEFLRPSSLIT-YDNPAFEPDVTTLTEPRSNVPSDEMDIILRLRP	285
Db	4140	-----PRPTPTGQTPTTPTTTTTTTPPTP-----P	4167
QY	286	ALTSRAGTVRPSRLGQRATMTFRSGTQAGAVHFHDISPLA-----PSPVEYLQ---	336
Db	4168	TGCTPTPTTPTTTTTTTPPTPTPTGQTGPPRTH--TSTAPLAEILTNSPPRESSPTQSR	4222
QY	337	-----PLVSATEDNGLFDIYADDIDPAMFY-----PSRPTTSANVSATYSPT-----	377

Db	4226	STSPLEFST	-----TILSTLPALMSTAPSPSTPTATTTSGCHTLLPBPSTTSP	4278
Qy	378	-----	ISASSTANTVPLTSW---DVPYTGPOITLPPSYMIVSP	419
Db	4279	PGPRGTGSSASAPPSIVQTTTSTAMPPLPPLST-PSI-IRTTGLRYPSSVLIC	4336	
Qy	420	-----	APASTOXIGHG-THYLL	436
Db	4337	VLANDTYAPGEVYNGTIGDTCYV	4361	

Search completed: October 17, 2003, 11:15:38
Job time : 45.3378 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 17, 2003, 10:59:19 ; Search time 266.694 Seconds
(without alignments)
1572.860 Million cell updates/sec

Title: US-08-913-644-4

Perfect score: 2405
Sequence: 1 MSHRAARRRRASVTDLKTT.....FLPKRRKRVYFADGFVAA 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
- 4: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
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- 15: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
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- 32: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2317.5	96.4	462	1	PCT-US00-33549-41

2	2317.5	96.4	462	25	US-09-991-053-4	Sequence 4, Appl1
3	2317.5	96.4	462	27	US-10-149-136-41	Sequence 41, Appl1
4	2317.5	96.4	462	29	US-10-301-260A-4	Sequence 4, Appl1
5	1973	82.0	463	1	PCT-US00-33549-54	Sequence 54, Appl1
6	1973	82.0	463	27	US-10-149-136-54	Sequence 54, Appl1
7	1486.5	61.8	464	1	PCT-US00-33549-66	Sequence 66, Appl1
8	1486.5	61.8	464	27	US-10-149-136-66	Sequence 66, Appl1
9	1460	60.7	471	1	PCT-US99-18810-9	Sequence 9, Appl1
10	1164.5	48.4	466	1	PCT-US00-33549-48	Sequence 48, Appl1
11	1164.5	48.4	466	27	US-10-149-136-48	Sequence 48, Appl1
12	1149.5	47.8	455	1	PCT-US00-33549-27	Sequence 27, Appl1
13	1149.5	47.8	455	27	US-10-149-136-27	Sequence 27, Appl1
14	1146.5	47.7	488	1	PCT-US03-04473-8	Sequence 8, Appl1
15	1146.5	47.7	488	1	PCT-US03-04473A-8	Sequence 8, Appl1
16	1146.5	47.7	488	1	PCT-US03-04474-8	Sequence 8, Appl1
17	1146.5	47.7	488	1	PCT-US03-04474A-8	Sequence 8, Appl1
18	1146.5	47.7	488	1	PCT-US03-04480-8	Sequence 8, Appl1
19	1146.5	47.7	488	1	PCT-US03-04480A-8	Sequence 8, Appl1
20	1146.5	47.7	488	1	PCT-US03-04516-8	Sequence 8, Appl1
21	1146.5	47.7	488	1	PCT-US03-04516A-8	Sequence 8, Appl1
22	1146.5	47.7	488	29	US-10-367-043-8	Sequence 8, Appl1
23	1146.5	47.7	488	29	US-10-367-043-8	Sequence 8, Appl1
24	1146.5	47.7	488	29	US-10-367-043-8	Sequence 8, Appl1
25	1146.5	47.7	488	29	US-10-367-043-8	Sequence 8, Appl1
26	1133.5	47.1	473	25	US-09-991-053-2	Sequence 2, Appl1
27	1133.5	47.1	473	29	US-10-301-260A-2	Sequence 2, Appl1
28	1131.5	47.0	470	1	PCT-US03-04473-7	Sequence 7, Appl1
29	1131.5	47.0	470	1	PCT-US03-04473A-7	Sequence 7, Appl1
30	1131.5	47.0	470	1	PCT-US03-04474-7	Sequence 7, Appl1
31	1131.5	47.0	470	1	PCT-US03-04474A-7	Sequence 7, Appl1
32	1131.5	47.0	470	1	PCT-US03-04480-7	Sequence 7, Appl1
33	1131.5	47.0	470	1	PCT-US03-04480A-7	Sequence 7, Appl1
34	1131.5	47.0	470	1	PCT-US03-04516-7	Sequence 7, Appl1
35	1131.5	47.0	470	1	PCT-US03-04516A-7	Sequence 7, Appl1
36	1131.5	47.0	470	29	US-10-367-043-7	Sequence 7, Appl1
37	1131.5	47.0	470	29	US-10-367-043-7	Sequence 7, Appl1
38	1131.5	47.0	470	29	US-10-367-043-7	Sequence 7, Appl1
39	1131.5	47.0	470	29	US-10-368-046-7	Sequence 7, Appl1
40	1131.5	47.0	473	1	PCT-US00-33549-34	Sequence 34, Appl1
41	1131.5	47.0	536	1	PCT-US03-04473A-10	Sequence 10, Appl1
42	1131.5	47.0	536	1	PCT-US03-04474-10	Sequence 10, Appl1
43	1131.5	47.0	536	1	PCT-US03-04474A-10	Sequence 10, Appl1
44	1131.5	47.0	536	1	PCT-US03-04474A-10	Sequence 10, Appl1
45	1131.5	47.0	536	1	PCT-US03-04474A-10	Sequence 10, Appl1

ALIGNMENTS

RESULT 1
PCT-US00-33549-41
Sequence 41, Application PC/TUS0033549
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Betteban
APPLICANT: Grey, Howard M.
TITLE OF INVENTION: Inducing Cellular Immune Responses to Human
TITLE OF INVENTION: Papillomavirus Using Peptide and Nucleic Acid
FILE REFERENCE: 018623-016110PC
CURRENT APPLICATION NUMBER: PCT/US00/33549
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/641,528
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41

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: LENGTH: 462
: TYPE: PRT
: ORGANISM: Human papillomavirus type 18
PCT-0500-33549-41

Query Match      96.4%; Score 2317.5; DB 1; Length 462;
Best Local Similarity 96.8%; Pred. No. 1.2e-186;
Matches 447; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

OY 1 MSHRAARRKRASTYDLKTKCKQSGTCCPDVNVKVEGTTLADKILQWSSLGIFLGIG 60
DB 1 MSHRAARRKRASTYDLKTKCKQSGTCCPDVNVKVEGTTLADKILQWSSLGIFLGIG 60
OY 61 TGSCTGRTGYIPLGGRSNTVVDGPTRPVPIEVGPTDPSIYTLIEDSSVYTSGAR 120
DB 61 TGSCTGRTGYIPLGGRSNTVVDGPTRPVPIEVGPTDPSIYTLIEDSSVYTSGAR 120
OY 121 TFGTSGFDITSAGTTTTPAVLDITPSSTSVSISTTFNPAFSDPSIIEVQTEVAGNV 180
DB 121 TFGTSGFDITSAGTTTTPAVLDITPSSTSVSISTTFNPAFSDPSIIEVQTEVAGNV 180
OY 121 TFGTSGFDITSAGTTTTPAVLDITPSSTSVSISTTFNPAFSDPSIIEVQTEVAGNV 180
DB 121 TFGTSGFDITSAGTTTTPAVLDITPSSTSVSISTTFNPAFSDPSIIEVQTEVAGNV 180
OY 181 FVGPTSGTGHYEELIPLQTFASSSGTGEPISTPLPYRRAVAGRLYSRAVOOVANPE 240
DB 181 FVGPTSGTGHYEELIPLQTFASSSGTGEPISTPLPYRRAVAGRLYSRAVOOVANPE 240
OY 241 FLTRPSSLITYDNPAFEVDITLTFEPNSNVPDSDFMIDILHRPALTSRGGYRFSRLG 300
DB 241 FLTRPSSLITYDNPAFEVDITLTFEPNSNVPDSDFMIDILHRPALTSRGGYRFSRLG 300
OY 301 ORATMFTRSQTQIGARVHFYHDISPIAPSPYIELQPLVSATEDNGLFDIYADDIDPAMP 360
DB 301 ORATMFTRSQTQIGARVHFYHDISPIAPSPYIELQPLVSATEDNGLFDIYADDIDPAMP 360
OY 361 VPSRPTSSAVSTSPITSSASSYSNTVPLTSSMDVVPYTGPDITLP-PTSVMPISPT 419
DB 361 VPSRPTSSAVSTSPITSSASSYSNTVPLTSSMDVVPYTGPDITLP-PTSVMPISPT 419
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DB 420 APASTQYIGIGHYHLYLMPLYYFIPKKRRKRVYFFADGFVAA 461

RESULT 2
US-09-991-053-4
: Sequence 4, Application US/09991053
: GENERAL INFORMATION:
: APPLICANT: Harrison, Stephen
: TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
: FILE REFERENCE: Harvard/Harrison 12687/1120
: CURRENT FILING DATE: 2001-11-21
: PRIOR APPLICATION NUMBER: US/09/520,781
: PRIOR FILING DATE: 2000-03-18
: PRIOR APPLICATION NUMBER: 60/125208
: PRIOR FILING DATE: 1999-03-18
: PRIOR APPLICATION NUMBER: 60/148544
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 462
: TYPE: PRT
: ORGANISM: Human papillomavirus type 18
US-09-991-053-4

Query Match      96.4%; Score 2317.5; DB 25; Length 462;
Best Local Similarity 96.8%; Pred. No. 1.2e-186;
Matches 447; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

OY 1 MSHRAARRKRASTYDLKTKCKQSGTCCPDVNVKVEGTTLADKILQWSSLGIFLGIG 60
DB 1 MSHRAARRKRASTYDLKTKCKQSGTCCPDVNVKVEGTTLADKILQWSSLGIFLGIG 60
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DB 1 MSHRAARRKRASTYDLKTKCKQSGTCCPDVNVKVEGTTLADKILQWSSLGIFLGIG 60
OY 61 TGSCTGRTGYIPLGGRSNTVVDGPTRPVPIEVGPTDPSIYTLIEDSSVYTSGAR 120
DB 61 TGSCTGRTGYIPLGGRSNTVVDGPTRPVPIEVGPTDPSIYTLIEDSSVYTSGAR 120
OY 121 TFGTSGFDITSAGTTTTPAVLDITPSSTSVSISTTFNPAFSDPSIIEVQTEVAGNV 180
DB 121 TFGTSGFDITSAGTTTTPAVLDITPSSTSVSISTTFNPAFSDPSIIEVQTEVAGNV 180
OY 181 FVGPTSGTGHYEELIPLQTFASSSGTGEPISTPLPYRRAVAGRLYSRAVOOVANPE 240
DB 181 FVGPTSGTGHYEELIPLQTFASSSGTGEPISTPLPYRRAVAGRLYSRAVOOVANPE 240
OY 241 FLTRPSSLITYDNPAFEVDITLTFEPNSNVPDSDFMIDILHRPALTSRGGYRFSRLG 300
DB 241 FLTRPSSLITYDNPAFEVDITLTFEPNSNVPDSDFMIDILHRPALTSRGGYRFSRLG 300
OY 301 ORATMFTRSQTQIGARVHFYHDISPIAPSPYIELQPLVSATEDNGLFDIYADDIDPAMP 360
DB 301 ORATMFTRSQTQIGARVHFYHDISPIAPSPYIELQPLVSATEDNGLFDIYADDIDPAMP 360
OY 361 VPSRPTSSAVSTSPITSSASSYSNTVPLTSSMDVVPYTGPDITLP-PTSVMPISPT 419
DB 361 VPSRPTSSAVSTSPITSSASSYSNTVPLTSSMDVVPYTGPDITLP-PTSVMPISPT 419
OY 420 APASTQYIGIGHYHLYLMPLYYFIPKKRRKRVYFFADGFVAA 461
DB 420 APASTQYIGIGHYHLYLMPLYYFIPKKRRKRVYFFADGFVAA 461

RESULT 3
US-10-149-136-41
: Sequence 41, Application US/10149136
: GENERAL INFORMATION:
: APPLICANT: Sette, Alessandro
: APPLICANT: Sidney, John
: APPLICANT: Southwood, Scott
: APPLICANT: Chesnut, Robert
: APPLICANT: Cells, Esteban
: APPLICANT: Grey, Howard M.
: TITLE OF INVENTION: Inducing Cellular Immune Responses to Human Papillomavirus
: FILE REFERENCE: 2060.010002
: CURRENT FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: US/10/149,136
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: WO PCT/US00/33549
: PRIOR FILING DATE: 2000-08-15
: PRIOR APPLICATION NUMBER: US 60/172,705
: PRIOR FILING DATE: 1999-12-10
: NUMBER OF SEQ ID NOS: 88
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 41
: LENGTH: 462
: TYPE: PRT
: ORGANISM: Human papillomavirus type 18
US-10-149-136-41

Query Match      96.4%; Score 2317.5; DB 27; Length 462;
Best Local Similarity 96.8%; Pred. No. 1.2e-186;
Matches 447; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

OY 1 MSHRAARRKRASTYDLKTKCKQSGTCCPDVNVKVEGTTLADKILQWSSLGIFLGIG 60
DB 1 MSHRAARRKRASTYDLKTKCKQSGTCCPDVNVKVEGTTLADKILQWSSLGIFLGIG 60
OY 61 TGSCTGRTGYIPLGGRSNTVVDGPTRPVPIEVGPTDPSIYTLIEDSSVYTSGAR 120
DB 61 TGSCTGRTGYIPLGGRSNTVVDGPTRPVPIEVGPTDPSIYTLIEDSSVYTSGAR 120
OY 121 TFGTSGFDITSAGTTTTPAVLDITPSSTSVSISTTFNPAFSDPSIIEVQTEVAGNV 180
DB 121 TFGTSGFDITSAGTTTTPAVLDITPSSTSVSISTTFNPAFSDPSIIEVQTEVAGNV 180
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Db      121 TTGTSGFDITSGATTTPAVLDITPSSVSISTTNFTNPASDPSEIIEVPOGEVAGNV 180
Qy      181 FVGTPTSGHGYEELIPLQTFASSGTGEPISSITPLTVRRVAGPRISRAYOQVSAVNE 240
Db      181 FVGTPTSGHGYEELIPLQTFASSGTGEPISSITPLTVRRVAGPRISRAYOQVSAVNE 240
Qy      241 FLTRPSSLTYNDNPAPEPVDITLTPEPRSNVPSDMDIIRLHRPALTSRGTVRFSRLG 300
Db      241 FLTRPSSLTYNDNPAPEPVDITLTPEPRSDVPSDMDIIRLHRPALTSRGTVRFSRLG 300
Qy      301 ORATMFTRSCTQIGARVHFYHDISPIAPSEYEIELOPLVSATEDNGLFDIYADDIDPAMP 360
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Qy      361 VPSRPTTSSAVSTYSPITSSASSYSNVTPLTSSMDVPVYTGPDITLP-PTSWPITVSP 419
Db      361 VPSRSTTSFAFFKYSPTISSASSYSNVTPLTSSMDVPVYTGPDITLPSTTSWPIVSP 420
Qy      420 APASTOYIGIGHYHYLMPLYYFIPIKKRRRVYFFADGFVAA 461
Db      421 APASTOYIGIGHYHYLMPLYYFIPIKKRRRVYFFADGFVAA 462

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RESULT 4
US-10-301-260A-4
; Sequence 4, Application US/10301260A
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen
; APPLICANT: Chen, Xiaojiang
; TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
; FILE REFERENCE: Harvard/Harrison 12687/1123
; CURRENT APPLICATION NUMBER: US/10/301,260A
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 09/520,822
; PRIOR FILING DATE: 2000-03-18
; PRIOR APPLICATION NUMBER: 60/125208
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/148544
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-10-301-260A-4

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Query Match      96.4%; Score 2317.5; DB 29; Length 462;
Best Local Similarity 96.8%; Pred. No. 1.2e-186;
Matches 447; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

Qy      1 MWSHRAARRKRAATVDLYKTCQSGCPCSDVNVKVGSTTLADKIILQWSSIGIFLGGLGIG 60
Db      1 MWSHRAARRKRAATVDLYKTCQSGCPCSDVNVKVGSTTLADKIILQWSSIGIFLGGLGIG 60
Qy      61 TSGGTGRTGYIPLGGRSNTVDVGPTRPPVIEPVPDPSPITVLTLEDSVYTSAGAPR 120
Db      61 TSGGTGRTGYIPLGGRSNTVDVGPTRPPVIEPVPDPSPITVLTLEDSVYTSAGAPR 120
Qy      121 TTGTSGFDITSGATTTPAVLDITPSSVSISTTNFTNPASDPSEIIEVPOGEVAGNV 180
Db      121 TTGTSGFDITSGATTTPAVLDITPSSVSISTTNFTNPASDPSEIIEVPOGEVAGNV 180
Qy      181 FVGTPTSGHGYEELIPLQTFASSGTGEPISSITPLTVRRVAGPRISRAYOQVSAVNE 240
Db      181 FVGTPTSGHGYEELIPLQTFASSGTGEPISSITPLTVRRVAGPRISRAYOQVSAVNE 240
Qy      241 FLTRPSSLTYNDNPAPEPVDITLTPEPRSNVPSDMDIIRLHRPALTSRGTVRFSRLG 300
Db      241 FLTRPSSLTYNDNPAPEPVDITLTPEPRSDVPSDMDIIRLHRPALTSRGTVRFSRLG 300

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Qy      301 ORATMFTRSCTQIGARVHFYHDISPIAPSEYEIELOPLVSATEDNGLFDIYADDIDPAMP 360
Db      301 ORATMFTRSCTQIGARVHFYHDISPIAPSEYEIELOPLVSATEDNGLFDIYADDIDPAMP 360
Qy      361 VPSRPTTSSAVSTYSPITSSASSYSNVTPLTSSMDVPVYTGPDITLP-PTSWPITVSP 419
Db      361 VPSRSTTSFAFFKYSPTISSASSYSNVTPLTSSMDVPVYTGPDITLPSTTSWPIVSP 420
Qy      420 APASTOYIGIGHYHYLMPLYYFIPIKKRRRVYFFADGFVAA 461
Db      421 APASTOYIGIGHYHYLMPLYYFIPIKKRRRVYFFADGFVAA 462

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RESULT 5
PCT-US00-33549-54
; Sequence 54, Application PC/TUS0033549
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Betteban
; APPLICANT: Grey, Howard M.
; APPLICANT: Bpimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Human
; TITLE OF INVENTION: Papillomavirus Using Peptide and Nucleic Acid
; FILE REFERENCE: 018623-016110PC
; CURRENT APPLICATION NUMBER: PCT/US00/33549
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/641,528
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 54
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Human papillomavirus type 45
PCT-US00-33549-54

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Query Match      82.0%; Score 1973; DB 1; Length 463;
Best Local Similarity 81.7%; Pred. No. 1.7e-157;
Matches 379; Conservative 33; Mismatches 48; Indels 4; Gaps 3;

Qy      1 MWSHRAARRKRAATVDLYKTCQSGCPCSDVNVKVGSTTLADKIILQWSSIGIFLGGLGIG 60
Db      1 MWSHRAARRKRAATVDLYKTCQSGCPCSDVNVKVGSTTLADKIILQWSSIGIFLGGLGIG 60
Qy      61 TSGGTGRTGYIPLGGRSNTVDVGPTRPPVIEPVPDPSPITVLTLEDSVYTSAGAPR 120
Db      61 TSGGTGRTGYIPLGGRSNTVDVGPTRPPVIEPVPDPSPITVLTLEDSVYTSAGAPR 120
Qy      121 TTGTSGFDITSGATTTPAVLDITPSSVSISTTNFTNPASDPSEIIEVPOGEVAGNV 180
Db      121 TTGTSGFDITSGATTTPAVLDITPSSVSISTTNFTNPASDPSEIIEVPOGEVAGNV 180
Qy      181 FVGTPTSGHGYEELIPLQTFASSGTGEPISSITPLTVRRVAGPRISRAYOQVSAVNE 240
Db      181 FVGTPTSGHGYEELIPLQTFASSGTGEPISSITPLTVRRVAGPRISRAYOQVSAVNE 240
Qy      241 FLTRPSSLTYNDNPAPEPVDITLTPEPRSNVPSDMDIIRLHRPALTSRGTVRFSRLG 300
Db      241 FLTRPSSLTYNDNPAPEPVDITLTPEPRSNVPSDMDIIRLHRPALTSRGTVRFSRLG 300
Qy      301 ORATMFTRSCTQIGARVHFYHDISPIAPSEYEIELOPLVSATEDNGLFDIYADDIDPAMP 360
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Qy      361 VPSRPTTSSAVSTYSPITSSASSYSNVTPLTSSMDVPVYTGPDITLP-PTSWPITVSP 417
Db      360 TPSTIRKSTYPRISLIMBSTAASSYSNVTPLTSSMDVPVYTGPDITLPSTHTPMPST 419

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QY 418 PTAASQYIGIHGTHYLMPLYIFPKRRKRVYFFADGVAA 461
DB 420 PTNASTTYIGIHGTHYLMPLYIFPKRRKRIPEFFADGVAA 463

RESULT 6
US-10-149-136-54
; Sequence 54, Application US/10149136
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard M.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Human Papillomavirus
; FILE REFERENCE: 2060 0100002
; CURRENT APPLICATION NUMBER: US/10/149,136
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: WO PCT/US00/33549
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/641,528
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Human papillomavirus type 45
US-10-149-136-54

Query Match 82.0%; Score 1973; DB 27; Length 463;
Best Local Similarity 81.7%; Pred. No. 1,7e-157;
Matches 379; Conservative 33; Mismatches 46; Indels 4; Gaps 3;

QY 1 MSHRAARRKRASTYDLYKTKQSGTQCPDVYKRVKVEGTTLADKILQMSLIGIFLGIG 60
DB 1 MSHRAARRKRASTYDLYKTKQSGTQCPDVYKRVKVEGTTLADKILQMSLIGIFLGIG 60
QY 61 TGSCTGRTGYIPLGSGNSNVVDGPPRPVIEPVGPTDPSIYTLIEDSSVVTSGAPRP 120
DB 61 TGSCTGRTGYIPLGSGNSNVVDGPPRPVIEPVGPTDPSIYTLIEDSSVVTSGAPRP 120
QY 121 TFGTSGFDIYSAAGTTTAVLDITPSSSTVSISTNTNPAFSDPSIIEVQTEVSGNV 180
DB 121 TFGTSGFDIYSAAGTTTAVLDITPSSSTVSISTNTNPAFSDPSIIEVQTEVSGNV 180
QY 121 TFGTSGFDIYSAAGTTTAVLDITPSSSTVSISTNTNPAFSDPSIIEVQTEVSGNV 180
DB 121 TFGTSGFDIYSAAGTTTAVLDITPSSSTVSISTNTNPAFSDPSIIEVQTEVSGNV 180
QY 181 FVGCTPTSGHGYEIPLOTFASSGTEPISSTPLPVRRVGRPLYSRAQOVSANPE 240
DB 181 FVGCTPTSGHGYEIPLOTFASSGTEPISSTPLPVRRVGRPLYSRAQOVSANPE 240
QY 241 FLTPSSLIYDNPAPFEPVDTTLTFEPRSNVPSDPMIDIRLHRPALTSRGTVRSRLG 300
DB 241 FLTPSSLIYDNPAPFEPVDTTLTFEPRSNVPSDPMIDIRLHRPALTSRGTVRSRLG 300
QY 241 FLTPSSLIYDNPAPFEPVDTTLTFEPRSNVPSDPMIDIRLHRPALTSRGTVRSRLG 300
DB 241 FLTPSSLIYDNPAPFEPVDTTLTFEPRSNVPSDPMIDIRLHRPALTSRGTVRSRLG 300
QY 301 QRAATMFRSGQIGARVHFYHDISPIASPEYIELQPLVSAETENGLEFDIYADIDPAMP 360
DB 301 QRAATMFRSGQIGARVHFYHDISPIASPEYIELQPLVSAETENGLEFDIYADIDPAMP 360
QY 301 QRAATMFRSGQIGARVHFYHDISPIASPEYIELQPLVSAETENGLEFDIYADIDPAMP 360
DB 301 QRAATMFRSGQIGARVHFYHDISPIASPEYIELQPLVSAETENGLEFDIYADIDPAMP 360
QY 361 VPSRPTSSAVSTYSPTISS--ASSYSNVVPLTSSMDVPPYTGPDITLPP--TSVMPIVS 417
DB 361 VPSRPTSSAVSTYSPTISS--ASSYSNVVPLTSSMDVPPYTGPDITLPP--TSVMPIVS 417
QY 418 PTAASQYIGIHGTHYLMPLYIFPKRRKRVYFFADGVAA 461
DB 420 PTNASTTYIGIHGTHYLMPLYIFPKRRKRIPEFFADGVAA 463

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PCT-US00-33549-66
; Sequence 66, Application PC/TUS0033549
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Human
; TITLE OF INVENTION: Papillomavirus Using Peptide and Nucleic Acid
; FILE REFERENCE: 018623-016110PC
; CURRENT APPLICATION NUMBER: PCT/US00/33549
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/641,528
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Human papillomavirus type 56
PCT-US00-33549-66

```

```

Query Match 61.8%; Score 1486.5; DB 1; Length 464;
Best Local Similarity 61.1%; Pred. No. 2.4e-116;
Matches 284; Conservative 68; Mismatches 108; Indels 5; Gaps 4;

QY 1 MSHRAARRKRASTYDLYKTKQSGTQCPDVYKRVKVEGTTLADKILQMSLIGIFLGIG 60
DB 1 MSHRAARRKRASTYDLYKTKQSGTQCPDVYKRVKVEGTTLADKILQMSLIGIFLGIG 60
QY 61 TGSCTGRTGYIPLGSGNSNVVDGPPRPVIEPVGPTDPSIYTLIEDSSVVTSGAPRP 120
DB 61 TGSCTGRTGYIPLGSGNSNVVDGPPRPVIEPVGPTDPSIYTLIEDSSVVTSGAPRP 120
QY 121 TFGTSGFDIYSAAGTTTAVLDITPSSSTVSISTNTNPAFSDPSIIEVQTEVSGNV 180
DB 121 TFGTSGFDIYSAAGTTTAVLDITPSSSTVSISTNTNPAFSDPSIIEVQTEVSGNV 180
QY 121 TFGTSGFDIYSAAGTTTAVLDITPSSSTVSISTNTNPAFSDPSIIEVQTEVSGNV 180
DB 121 TFGTSGFDIYSAAGTTTAVLDITPSSSTVSISTNTNPAFSDPSIIEVQTEVSGNV 180
QY 181 FVGCTPTSGHGYEIPLOTFASSGTEPISSTPLPVRRVGRPLYSRAQOVSANPE 240
DB 181 FVGCTPTSGHGYEIPLOTFASSGTEPISSTPLPVRRVGRPLYSRAQOVSANPE 240
QY 181 LISTPTSGHGYEIPLOTFASSGTEPISSTPLPVRRVGRPLYSRAQOVSANPE 240
DB 181 LISTPTSGHGYEIPLOTFASSGTEPISSTPLPVRRVGRPLYSRAQOVSANPE 240
QY 241 FLTPSSLIYDNPAPFEPVDTTLTFEPRSNVPSDPMIDIRLHRPALTSRGTVRSRLG 300
DB 241 FLTPSSLIYDNPAPFEPVDTTLTFEPRSNVPSDPMIDIRLHRPALTSRGTVRSRLG 300
QY 241 FLTPSSLIYDNPAPFEPVDTTLTFEPRSNVPSDPMIDIRLHRPALTSRGTVRSRLG 300
DB 241 FLTPSSLIYDNPAPFEPVDTTLTFEPRSNVPSDPMIDIRLHRPALTSRGTVRSRLG 300
QY 301 QRAATMFRSGQIGARVHFYHDISPIASPEYIELQPLVSAETENGLEFDIYADIDPAMP 357
DB 301 QRAATMFRSGQIGARVHFYHDISPIASPEYIELQPLVSAETENGLEFDIYADIDPAMP 357
QY 301 QRAATMFRSGQIGARVHFYHDISPIASPEYIELQPLVSAETENGLEFDIYADIDPAMP 357
DB 301 QRAATMFRSGQIGARVHFYHDISPIASPEYIELQPLVSAETENGLEFDIYADIDPAMP 357
QY 358 AMPVPSRPTSSAVSTYSPTISSASYSNTVPLTSSMDVPPYTGPDITLPP--TSVMPIV 416
DB 358 AMPVPSRPTSSAVSTYSPTISSASYSNTVPLTSSMDVPPYTGPDITLPP--TSVMPIV 416
QY 360 GLSSQVATPSAHLPIKPSLTLSFASNTNTVAPLGNWMEPPVSGPDIVLPTGSGTNPV 419
DB 360 GLSSQVATPSAHLPIKPSLTLSFASNTNTVAPLGNWMEPPVSGPDIVLPTGSGTNPV 419
QY 417 SPTAPASTQYIGIHGTHYLMPLYIFPKRRKRVYFFADGVAA 461
DB 420 POSPYDVTHVYIGSSSFALMPYVFFRRRRKRIPEFFADGVAA 464

```

RESULT 7

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; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard M.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Human Papillomavirus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0100002
; CURRENT APPLICATION NUMBER: US/10/149,136
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: WO PCT/US00/33549
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/641,528
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 464
; TYPE: PRN
; ORGANISM: Human papillomavirus type 56
US-10-149-136-66

```

```

Query Match      61.8%; Score 1486.5; DB 27; Length 464;
Best Local Similarity 61.1%; Pred. No. 2.4e-116;
Matches 284; Conservative 68; Mismatches 108; Indels 5; Gaps 4;

```

```

QY 1 MSHRAARRKRAVTDLYKTKCKOSGTCPSDVNKKVEGTTLADKILQMSLGLFGLGIG 60
DB 1 MSHRAARRKRAVTDLYKTKCKOSGTCPSDVNKKVEGTTLADKILQMSLGLFGLGIG 60
QY 61 TSGTGGRGTGYIPLGGSNTYVDVGPTRPVVIEPVGPDIPSVTLIEDSSVYTSQAPRP 120
DB 61 TSGTGGRGTGYIPLGGSNTYVDVGPTRPVVIEPVGPDIPSVTLIEDSSVYTSQAPRP 120
QY 121 TFGTSGFDITSAAGTTTTPAVLDTTPSSSTVSISTNTFNPAFSDPSIIEVPGTGEVSNV 180
DB 121 TFGTSGFDITSAAGTTTTPAVLDTTPSSSTVSISTNTFNPAFSDPSIIEVPGTGEVSNV 180
QY 121 NFGSGGFETTSSTTTPAVLDTTPSSSTVHVSHTITNPLFIDPVIEARPGEGVSGNI 180
DB 121 NFGSGGFETTSSTTTPAVLDTTPSSSTVHVSHTITNPLFIDPVIEARPGEGVSGNI 180
QY 181 FVGTPTSGTHGYEIPLOTFPAGSGTGEBPISSTPLPTVRRVACPRLYSRAVOOVSAANPE 240
DB 181 FVGTPTSGTHGYEIPLOTFPAGSGTGEBPISSTPLPTVRRVACPRLYSRAVOOVSAANPE 240
QY 181 LSTPTSGIHSYEIPMOQTFVAVGSGTEPISSTPIGFRRIARPLYRKAFQOVKVTDP 240
DB 181 LSTPTSGIHSYEIPMOQTFVAVGSGTEPISSTPIGFRRIARPLYRKAFQOVKVTDP 240
QY 241 FLTRPSLLTYDNPAPFEPVDTTLTFEPRSNVPSDSDMDIIRLRPALTSRGGVRRSRIG 300
DB 241 FLTRPSLLTYDNPAPFEPVDTTLTFEPRSNVPSDSDMDIIRLRPALTSRGGVRRSRIG 300
QY 241 FLDRPATLVASADNPLEGDTSLAFSGVAPDPDMNVALHRPAFTTRKGGVRRSRIG 300
DB 241 FLDRPATLVASADNPLEGDTSLAFSGVAPDPDMNVALHRPAFTTRKGGVRRSRIG 300
QY 301 QRATMFTSGTQIGARVHFYHDISPIASPEYIELOPLVSATED-NGLEPDIVA--DDIDP 357
DB 301 QRATMFTSGTQIGARVHFYHDISPIASPEYIELOPLVSATED-NGLEPDIVA--DDIDP 357
QY 301 RKATIGTRGTOIGARVHYHYDISPIAQAE-TEMQPLSANNSPGLVDIVANIDDEAP 359
DB 301 RKATIGTRGTOIGARVHYHYDISPIAQAE-TEMQPLSANNSPGLVDIVANIDDEAP 359
QY 358 AMPVPRPTTSSAVSTYSPISASSTYNTVPLTSSMDVPTVGTGDTILPP-TSVWPIV 416
DB 358 AMPVPRPTTSSAVSTYSPISASSTYNTVPLTSSMDVPTVGTGDTILPP-TSVWPIV 416
QY 417 SPTAPASTOYIGIGHYHYLMPLYFLPKRRKRVPRFFADGFAA 461
DB 417 SPTAPASTOYIGIGHYHYLMPLYFLPKRRKRVPRFFADGFAA 461
QY 420 POSPYVTHDVIYIGSSPALMPYFFRRRRKRRIPIFFADGVAA 464
DB 420 POSPYVTHDVIYIGSSPALMPYFFRRRRKRRIPIFFADGVAA 464

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RESULT 9
PCT-US99-18810-9
; Sequence 9, Application PC/TUS9918810
; GENERAL INFORMATION:
; APPLICANT: Indiana University
; APPLICANT: Brown, Daron R.
; APPLICANT: McClovey, Tracy L.
; APPLICANT: Bryan, Janine T.
; APPLICANT: Fife, Kenneth H.
; TITLE OF INVENTION: Purified Human Papillomavirus
; FILE REFERENCE: AKTI 9835 PCT
; CURRENT APPLICATION NUMBER: PCT/US99/18810
; PRIOR FILING DATE: 1999-08-17
; EARLIER APPLICATION NUMBER: US 09/135,241
; EARLIER FILING DATE: 1998-08-17

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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 9
; LENGTH: 471
; TYPE: PRN
; ORGANISM: Human Papillomavirus 83
PCT-US99-18810-9

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```

Query Match      60.7%; Score 1460; DB 1; Length 471;
Best Local Similarity 62.0%; Pred. No. 4.3e-114;
Matches 298; Conservative 61; Mismatches 90; Indels 32; Gaps 10;

```

```

QY 2 VSHRAARRKRAVTDLYKTKCKOSGTCPSDVNKKVEGTTLADKILQMSLGLFGLGIG 61
DB 1 MSHVRRRRKRAVTDLYKTKCKOSGTCPSDVNKKVEGTTLADKILQMSLGLFGLGIG 60
QY 62 GSGTGGRGTGYIPLGGSNTYVDVGPTRPVVIEPVGPDIPSVTLIEDSSVYTSQAPRP 120
DB 62 GSGTGGRGTGYIPLGGSNTYVDVGPTRPVVIEPVGPDIPSVTLIEDSSVYTSQAPRP 120
QY 121 TFGTSGFDITSAAGTTTTPAVLDTTPSSSTVSISTNTFNPAFSDPSIIEVPGTGEVSNV 180
DB 121 TFGTSGFDITSAAGTTTTPAVLDTTPSSSTVSISTNTFNPAFSDPSIIEVPGTGEVSNV 180
QY 181 FVGTPTSGTHGYEIPLOTFPAGSGTGEBPISSTPLPTVRRVACPRLYSRAVOOVSA 237
DB 181 FVGTPTSGTHGYEIPLOTFPAGSGTGEBPISSTPLPTVRRVACPRLYSRAVOOVSA 237
QY 238 NPEFLRPSLLTYDNPAPFEPVDTTLTFEPRSNVPSDSDMDIIRLRPALTSRGGVRRSRIG 295
DB 238 NPEFLRPSLLTYDNPAPFEPVDTTLTFEPRSNVPSDSDMDIIRLRPALTSRGGVRRSRIG 295
QY 241 DSAPMSNPASFTYDNPVDP-DETIIFEPRLNPNPDPDLIVSLHRPALRAGTVR 299
DB 241 DSAPMSNPASFTYDNPVDP-DETIIFEPRLNPNPDPDLIVSLHRPALRAGTVR 299
QY 296 FSLRGATMFTSGTQIGARVHFYHDISPIASPEYIELOPLVSATEDNGLEPDIVADP 355
DB 296 FSLRGATMFTSGTQIGARVHFYHDISPIASPEYIELOPLVSATEDNGLEPDIVADP 355
QY 300 VSNVQGRATLRISGQIGARVHFYHDISPIPT-ESTIEQLEPVSANTSLDITADY 358
DB 300 VSNVQGRATLRISGQIGARVHFYHDISPIPT-ESTIEQLEPVSANTSLDITADY 358
QY 356 DPAMPVPRPTTSS-AVSTYSPISASSTYNTVPLTSSMDVPTVGTGDTI----- 405
DB 356 DPAMPVPRPTTSS-AVSTYSPISASSTYNTVPLTSSMDVPTVGTGDTI----- 405
QY 406 -----TLPTSVWPIVSPFAPASTOYIGIGHYHYLMPLYFLPKRRKRVPRFFADGFA 460
DB 406 -----TLPTSVWPIVSPFAPASTOYIGIGHYHYLMPLYFLPKRRKRVPRFFADGFA 460
QY 419 MPADPSVPVPSNIP-----QSVFIDGTDIYLLPNYFFPKRRKRHYVADGVAA 469
DB 419 MPADPSVPVPSNIP-----QSVFIDGTDIYLLPNYFFPKRRKRHYVADGVAA 469
QY 461 A 461
DB 470 A 470

```

```

RESULT 10
PCT-US00-33549-48
; Sequence 48, Application PC/TUS0033549
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard M.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Human Papillomavirus Using Peptide and Nucleic Acid
; FILE REFERENCE: 018623-016110PC
; CURRENT APPLICATION NUMBER: PCT/US00/33549
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/641,528
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48

```

1 LENGTH: 466
 2 TYPE: PRT
 3 ORGANISM: Human papillomavirus type 31
 4 PCT-US00-33549-48
 5
 6 Query Match 48.4%; Score 1164.5; DB 1; Length 466;
 7 Best Local Similarity 50.6%; Pred. No. 4,3e-89;
 8 Matches 247; Conservative 77; Mismatches 115; Indels 49; Gaps 14;
 9
 10 QY 1 MWSHRARR-KRASVTDLYTKCKGSGTCDSDVYNKVEGTTLADKILQWSSLGIFLGIGI 59
 11 Db 1 MRSKSTRKTRKASATOLYQTCAGATGCSVDYIPKIEHTTIADQILRYGSMGVFGLGI 60
 12 QY 60 GTSGSTGRTGYIPLGGRNTYVDVG-PRRPVVIEPVVPTDPSITYTLIEDSSVYTSAGP 118
 13 Db 61 GSGSGTGRTGYVPISTRPSTVSEASIPRPVSDIPVGLDPSIYSLVEESGIVDVGAP 120
 14 QY 119 RPT-FTGTSGEDITSAGTTPPAVLADIPPSSTSVSISTNTFTNPAFSDPSIIEVPQTGEV 176
 15 Db 121 APIPIRPTTSGEDITATDTPPAILDVT-----SVST--HENPRTTDSVGLPPTPAEL 172
 16 QY 177 SGANFVGPTSGTGHGEEIPIQTFPSSGTGEEPISSTPLPVYRVVAGPRLYSRAYQOVSV 236
 17 Db 173 SGHLTSSSSISITHYEEIPIQDTFTYSTNNENITSTPIGPYRRPARLIGYSKATQOVKV 232
 18 QY 237 ANPELTTPSSSLITDNPAAFEV--DTLTTEPRSN--VPDSDFMILRLHRAALTSRRG 292
 19 Db 233 IDPFLSLAPKOLITYENPAVEYTVNAEESLYFSNTSHINAPDDPEIDIALHRAALTSRRN 292
 20 QY 293 TVRFSLQARMTFTRSQTQIGARVHYFYHIDISPIASPPEYIELOPL-----VSATEDNGI 347
 21 Db 293 TVRSRLGNKQTLRRRSCTIGARVHYFYHIDISINAGSIEQPLGASATTTSTLNDGL 352
 22 QY 348 FDIYAD-----DIDPAMPVPSRPTTSSAVSTYPTTSSASSYSNVTYPLTSSMD 396
 23 Db 353 YDIYADTDFEYDTPATHNVSPSTAVOS---TSAVAYPT-----NTVPLSTGEG 400
 24 QY 397 VPYVAGPDTLT--PRTSWPIVSPFAPASTQY-IGHGHYIYMLPYIYIPKRRKVPPE 453
 25 Db 401 IPISGPPVPIEHAPTOVPP--PLAPTPQVSIFFVGDGFYLIHPSYMLKRRKRVSYSF 458
 26 QY 454 FADGEVAA 461
 27 Db 459 FTDVSVA 466
 28
 29 RESULT 11
 30 US-10-149-136-48
 31 Sequence 48, Application US/10149136
 32 GENERAL INFORMATION:
 33 APPLICANT: Sette, Alessandro
 34 APPLICANT: Sidney, John
 35 APPLICANT: Southwood, Scott
 36 APPLICANT: Chesnut, Robert
 37 APPLICANT: Cells, Esteban
 38 APPLICANT: Grey, Howard M.
 39 TITLE OF INVENTION: Inducing Cellular Immune Responses to Human Papillomavirus
 40 TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
 41 FILE REFERENCE: 2000.0100002
 42 CURRENT APPLICATION NUMBER: US/10/149,136
 43 CURRENT FILING DATE: 2000-12-11
 44 PRIOR APPLICATION NUMBER: WO PCT/US00/33549
 45 PRIOR FILING DATE: 2000-12-11
 46 PRIOR APPLICATION NUMBER: US 09/641,528
 47 PRIOR FILING DATE: 2000-08-15
 48 PRIOR APPLICATION NUMBER: US 60/172,705
 49 PRIOR FILING DATE: 1999-12-10
 50 NUMBER OF SEQ ID NOS: 88
 51 SOFTWARE: PatentIn version 3.1
 52 SEQ ID NO 48
 53 LENGTH: 466
 54 TYPE: PRT
 55 ORGANISM: Human papillomavirus type 31

Query Match	48.4%	Score 1164.5	DB 27	Length 466
Best Local Similarity	50.6%	Pred. No. 4.3e-89		
Matches 247	Conservative 77	Mismatches 115	Indels 49	Gaps 14
Query	1	MVSHRAAR-RRASVTDLYKTKOSGTCPSDPVNVKVEETITLADKTLKLOSSIGIFLGIGI	59	
Db	1	MRSRSTRRTKRRASATOLYQTKKAAGTCPSDVIPPIEHTTTIADQLLRKSGMVGFFGGIGI	60	
QY	60	GTGSGTGRTGYIFPLGSGRNTVVDVG-PTRPVYIEPVYPPDPSIVTLIEDSSVYTSQAP	118	
Db	61	GSGSGTGRTGYIVLSTPSTVSEASTIRRPYIDPGLDPSIVLSESGIYDVAP	120	
QY	119	RPT--FTGTSGFDITSAGTTTPAVLDTPSSTSVSISTTFTNTPAFSDPSIIEVPQTGEV	176	
Db	121	APIRHPTTSGFDIATVADTTPALIDVY-----SVST--HENPTFTDPVLIQPTPAET	172	
QY	177	SGNFVFGPTSGTGYEIRPIQOTFASSTGTEPISSTPLPVYRRVARGRLTSRAQQVSY	236	
Db	173	SGHLILSSSSISTHYEEIPMDTETIVSTNNNTTSSTPIPVRRPARGLTSKAAQQVKY	232	
QY	237	ANPEELTPSSLIITYVNDPAFEPV--DTLTGFEPRSN--VPDSDMDIIRLRPALTSRRG	292	
Db	233	IDPFLSLAKPLITYENAYETVNAEESLYESNTHNAPDPDFDIATLRPALTSRRN	292	
QY	293	TVRRSLRGQRATMFTRRSGTQIGARVHYHDISPIAPSEVYELQPL----VSATEDNGL	347	
Db	293	TVRRSLRGNKQTLTRSGATIGARVHYHDISSINPADESIEMDPIGASATTTSLINDGL	352	
QY	348	FDIYAD-----DIDPAMPSPRPTSSANSTVSPFISSASSVSNTPVPLTSSMD	396	
Db	353	YDIYADDFIVDTPTATHVSPSTAAQS---TSAVASAVPT-----NTVPLSTGPD	400	
QY	397	VPVYTGPDITL--PPTSVPIVSPTPAPASTQY-IGINHTHYLWPLYYFIKKRRKYVF	453	
Db	401	IPISGPPVPIEHNAPYQYFPF--PLAPYTPQVSIYFDGDDYLLHSHYYMLKRRRRVSYF	458	
QY	454	FADGFVAA 461		
Db	459	FTDVSVA 466		
RESULT 12				
PCT-US00-33549-27				
Sequence 27, Application PC/TUS0033549				
GENERAL INFORMATION:				
APPLICANT: Sette, Alessandro				
APPLICANT: Sidney, John				
APPLICANT: Southwood, Scott				
APPLICANT: Chesnut, Robert				
APPLICANT: Celis, Esteban				
APPLICANT: Grey, Howard M.				
APPLICANT: EpiImmune Inc.				
TITLE OF INVENTION: Inducing Cellular Immune Responses to Human Papillomavirus Using Peptide and Nucleic Acid				
TITLE OF INVENTION: Compositions				
FILE REFERENCE: 018623-016110PC				
CURRENT APPLICATION NUMBER: PCT/US00/33549				
CURRENT FILING DATE: 2000-12-11				
PRIOR APPLICATION NUMBER: US 60/172,705				
PRIOR FILING DATE: 1999-12-10				
PRIOR APPLICATION NUMBER: US 09/641,528				
PRIOR FILING DATE: 2000-08-15				
NUMBER OF SEQ ID NOS: 86				
SOFTWARE: PatentIn Ver. 2.1				
SEQ ID NO 27				
LENGTH: 455				
TYPE: PRT				
ORGANISM: Human papillomavirus type 11				
PCT-US00-33549-27				
Query Match	47.8%	Score 1149.5	DB 1	Length 455

Matches 237: Conservative 71: Mismatches 128: Indels 41: Gaps 11:

```

OY 6 AARRRASVLDYKTCOSGTCPSDVNKKVEGTTLADKILQWSSIGIFLAGIGTSGGT 65
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7 AKRTRRASATQLYKTCOSGTCPSDIPKVEGKTADQILQYGSWGVFGGIGTSGGT 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 66 GGRGYIPLGGRSTNVVD-VGPTRPVIEVGPDPDSIVTLIEDSSVYTSGARPTFT 123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 GGRGYIPLGGRSTNVVD-VGPTRPVIEVGPDPDSIVTLIEDSSVYTSGARPTFT 126
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 124 --GTSGPDITSAGTTPAVLDITPSSSVSISTNTFTNPAFSDPSIIEVPQTGEVSGNVF 181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 127 PPDVSGFSTITSTDTTPALIDINNTVTV-----TTHNNPTTDSVLOPPPTAETGHT 182
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 182 VGPPTSGTHGYEELPLOTFASSGTEEPISSTPLPTVRVAGPRLYSRAYQVSVANPEF 241
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 183 LSSSTISTHNEEELPMDTFIVSTNPNVTSTPTIGSRPVARLGLSRTTQOVKVDPAF 242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 242 LTRPSLITVNDPAFE--PVDTTLFEPRSN----VPDSMDIIRLHRPALTSRGTVR 295
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 243 VTPPKLITVNDPAFEGIDVNTLYFPNDNSINIADPDLIDIALHRPALTSRGTVR 302
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 296 FSRIGORATWPTRSQTQIGARVHFYHDISPIAPSEPEYIELQPLVSATE----- 343
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 303 YSRIGNKQTLTRSGKSGAKVHYDLSINPAFE-IELQITPSTYTTTSHASPTSI 361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 344 DNGLFDIADIDP---AMPVPSRPTSSAVSTSPITSSASSYSNVTVPILTSMVDVY 400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 362 NNGLYDIADDFIDTFTTVPVPSIPSTS--LSGYIP-----ANTTIIPGGAYNIPLV 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 401 TGPDITLPTSWPVIPTAPASQY-IGIHGTHYLYPLLYFPKRRKRPVPEAD 456
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 412 SGDPITWTQTSLPIYVGSPOYITLIADGDFYLPSTYMLKRRKRLPIFFSD 468
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 15.

PCT-US03-04473A-8

: Sequence 8, Application PC/TUS0304473A

: GENERAL INFORMATION:

: APPLICANT: NOVAVAX, INC., et al.

: TITLE OF INVENTION: Optimization of Gene Sequences of

: TITLE OF INVENTION: Chimeric Virus-Like Particles for Expression in Insect Cells

: FILE REFERENCE: 44149-4PCI

: CURRENT APPLICATION NUMBER: PCT/US03/04473A

: PRIOR FILING DATE: 2003-02-14

: PRIOR APPLICATION NUMBER: US 60/356,119

: PRIOR FILING DATE: 2002-02-14

: PRIOR APPLICATION NUMBER: US 60/356,161

: PRIOR FILING DATE: 2002-02-14

: PRIOR APPLICATION NUMBER: US 60/356,118

: PRIOR FILING DATE: 2002-02-14

: PRIOR APPLICATION NUMBER: US 60/356,133

: PRIOR FILING DATE: 2002-02-14

: PRIOR APPLICATION NUMBER: US 60/356,157

: PRIOR FILING DATE: 2002-02-14

: PRIOR APPLICATION NUMBER: US 60/356,156

: PRIOR FILING DATE: 2002-02-14

: PRIOR APPLICATION NUMBER: US 60/356,123

: PRIOR FILING DATE: 2002-02-14

: PRIOR APPLICATION NUMBER: US 60/356,113

: PRIOR FILING DATE: 2002-02-14

: PRIOR APPLICATION NUMBER: US 60/356,154

: PRIOR FILING DATE: 2002-02-14

: PRIOR APPLICATION NUMBER: US 60/356,135

: Remaining Prior Application data removed - See File Wrapper or PALM.

: NUMBER OF SEQ ID NOS: 13

: SOFTWARE: FastSeq for Windows Version 4.0

: SEQ ID NO 8

: LENGTH: 488

: TYPE: PRT

: ORGANISM: Artificial Sequence

: FEATURE:

: OTHER INFORMATION: HPV-16 L2/E7 fusion protein
PCT-US03-04473A-8

Query Match 47.7%, Score 1146.5; DB 1; Length 488;

Best Local Similarity 49.7%, Pred. No. 1.56-87;

Matches 237: Conservative 71: Mismatches 128: Indels 41: Gaps 11:

```

OY 6 AARRRASVLDYKTCOSGTCPSDVNKKVEGTTLADKILQWSSIGIFLAGIGTSGGT 65
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7 AKRTRRASATQLYKTCOSGTCPSDIPKVEGKTADQILQYGSWGVFGGIGTSGGT 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 66 GGRGYIPLGGRSTNVVD-VGPTRPVIEVGPDPDSIVTLIEDSSVYTSGARPTFT 123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 GGRGYIPLGGRSTNVVD-VGPTRPVIEVGPDPDSIVTLIEDSSVYTSGARPTFT 126
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 124 --GTSGPDITSAGTTPAVLDITPSSSVSISTNTFTNPAFSDPSIIEVPQTGEVSGNVF 181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 127 PPDVSGFSTITSTDTTPALIDINNTVTV-----TTHNNPTTDSVLOPPPTAETGHT 182
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 182 VGPPTSGTHGYEELPLOTFASSGTEEPISSTPLPTVRVAGPRLYSRAYQVSVANPEF 241
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 183 LSSSTISTHNEEELPMDTFIVSTNPNVTSTPTIGSRPVARLGLSRTTQOVKVDPAF 242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 242 LTRPSLITVNDPAFE--PVDTTLFEPRSN----VPDSMDIIRLHRPALTSRGTVR 295
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 243 VTPPKLITVNDPAFEGIDVNTLYFPNDNSINIADPDLIDIALHRPALTSRGTVR 302
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 296 FSRIGORATWPTRSQTQIGARVHFYHDISPIAPSEPEYIELQPLVSATE----- 343
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 303 YSRIGNKQTLTRSGKSGAKVHYDLSINPAFE-IELQITPSTYTTTSHASPTSI 361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 344 DNGLFDIADIDP---AMPVPSRPTSSAVSTSPITSSASSYSNVTVPILTSMVDVY 400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 362 NNGLYDIADDFIDTFTTVPVPSIPSTS--LSGYIP-----ANTTIIPGGAYNIPLV 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 401 TGPDITLPTSWPVIPTAPASQY-IGIHGTHYLYPLLYFPKRRKRPVPEAD 456
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 412 SGDPITWTQTSLPIYVGSPOYITLIADGDFYLPSTYMLKRRKRLPIFFSD 468
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Search completed: October 17, 2003, 11:13:21
Job time : 268.694 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 17, 2003, 10:47:38 ; Search time 14.2872 Seconds
(without alignments)
1517.395 Million cell updates/sec

Title: US-08-913-644-4

Perfect score: 2405
Sequence: 1 MVSHRAARRKASVTDLTKT.....FLPKRRRVPEFADGVAA 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2317.5	96.4	VL2_HPV18	P06793 human papill
2	1973	82.0	VL2_HPV45	P36761 human papill
3	1716	71.4	VL2_HPVME	P27965 human papill
4	1710.5	71.1	VL2_HPV70	P50801 human papill
5	1686.5	70.1	VL2_HPV39	P24839 human papill
6	1550	64.4	VL2_HPV29	P50800 human papill
7	1532.5	63.7	VL2_HPV10	P36747 human papill
8	1530	63.6	VL2_HPV30	P36786 human papill
9	1529	63.6	VL2_HPV53	P36784 human papill
10	1515	63.0	VL2_HPV28	P50799 human papill
11	1513	62.9	VL2_HPV03	P36744 human papill
12	1493.5	62.1	VL2_HPV66	O80960 human papill
13	1486.5	61.8	VL2_HPV56	P36784 human papill
14	1483.5	61.7	VL2_HPV26	P26539 human papill
15	1466.5	61.0	VL2_HPV51	P25467 human papill
16	1457	60.6	VL2_HPV21	P36755 human papill
17	1423.5	59.2	VL2_HPV27	P22164 human papill
18	1387.5	57.7	VL2_HPV57	O80953 human papill
19	1384	57.5	VL2_HPV61	P17389 human papill
20	1164.5	48.4	VL2_HPV31	O02275 human papill
21	1158	48.1	VL2_HPV13	P04013 human papill
22	1149.5	47.8	VL2_HPV11	O80939 human papill
23	1143.5	47.5	VL2_HPV55	O80918 human papill
24	1139.5	47.4	VL2_HPV44	P22165 rhesus papill
25	1138.5	47.3	VL2_RHPV1	O84287 human papill
26	1137	47.3	VL2_HPV6A	P36763 human papill
27	1133.5	47.1	VL2_HPV52	P03107 human papill
28	1133.5	47.1	VL2_HPV16	P03106 human papill
29	1131	47.0	VL2_HPV6B	O81023 human papill
30	1122.5	46.7	VL2_HPV54	P27235 human papill
31	1117	46.4	VL2_HPV42	P26538 human papill
32	1116.5	46.4	VL2_HPV58	P06418 human papill
33	1114	46.3	VL2_HPV33	

34	1110	46.2	463	1	VL2_PCPV1	O02276 pygmy chimp
35	1108.5	46.1	456	1	VL2_HPV07	P36745 human papill
36	1088	45.2	472	1	VL2_HPV34	P36758 human papill
37	1087.5	45.2	476	1	VL2_HPV32	P36757 human papill
38	1069	44.4	467	1	VL2_HPV40	P36760 human papill
39	1060	44.1	469	1	VL2_HPV35	P27234 human papill
40	667	27.7	519	1	VL2_HPV23	P50797 human papill
41	642.5	26.7	519	1	VL2_HPV14	P36749 human papill
42	640.5	26.6	527	1	VL2_HPV38	O80912 human papill
43	639.5	26.6	533	1	VL2_HPV09	P36746 human papill
44	639	26.6	534	1	VL2_HPV37	O80905 human papill
45	635	26.4	524	1	VL2_HPV22	P50796 human papill

ALIGNMENTS

```
RESULT 1
VL2_HPV18          STANDARD;          PRT;   462 AA.
ID              VL2_HPV18
AC P06793;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE Minor capsid protein L2.
GN L2.
OS Human Papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87283882; PubMed=3039146;
RA Cole S.T., Danos O.;
RT "Nucleotide sequence and comparative analysis of the human
RT papillomavirus type 18 genome. Phylogeny of papillomaviruses and
RT repeated structure of the E6 and E7 gene products."
RL J. Mol. Biol. 193:599-608(1987).
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DR EMBL; X05015; CA28670.1; -.
DR PIR; B26251; P2WL18.
DR InterPro; IPR000784; Late_L2.
DR Pfam; PF00513; late_protein_L2; 1.
KW Coat protein; late protein.
SQ
SEQUENCE 462 AA; 49596 MW; 6482C186CCA3D7E4 CRC64;
Query Match 96.4%; Score 2317.5; DB 1; Length 462;
Best Local Similarity 96.8%; Pred. No. 3.1e-135;
Matches 447; Conservative 5; Mismatches 9; Indels 1; Gaps 1;
QY 1 MVSHRAARRKASVTDLTKTKCKSGCPSPVYKKEVETTLADKILQMSIGIFLGIGIG 60
Db 1 MVSHRAARRKASVTDLTKTKCKSGCPSPVYKKEVETTLADKILQMSIGIFLGIGIG 60
QY 1 TSGGTGRTGYILGGRSNTVVDGPTRPVYIEPVGPTPSTVTLIEDSVYSGAPRP 120
Db 1 TSGGTGRTGYILGGRSNTVVDGPTRPVYIEPVGPTPSTVTLIEDSVYSGAPRP 120
QY 1 TFGTSGFDITSGAGTTTTPAVLDITPSSSTVSISTNFTNPAFSDPSIIEVPGGEVAGNV 180
Db 1 TFGTSGFDITSGAGTTTTPAVLDITPSSSTVSISTNFTNPAFSDPSIIEVPGGEVAGNV 180
QY 1 FVGTPTSGTHGYEIEIPLOTFASSGTGGEPISSPLTVRRVAPRILYSRAVQVSYANPE 240
Db 1 FVGTPTSGTHGYEIEIPLOTFASSGTGGEPISSPLTVRRVAPRILYSRAVQVSYANPE 240
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QY 241 FLTRPSSLLTYDNPAFEVDTTLTFEPNSNVPDSDFMIDILHRPALTSRRGTVAFSRLG 300
DB 241 FLTRPSSLLTYDNPAFEVDTTLTFEPNSNVPDSDFMIDILHRPALTSRRGTVAFSRLG 300
QY 301 ORATMFRTSSGQIOGARVHFYHDISPIAPSPYEILOPLVSAITEDGLFADDDIDPAMP 360
DB 301 ORATMFRTSSGQIOGARVHFYHDISPIAPSPYEILOPLVSAITEDGLFADDDIDPAMP 360
QY 361 VPSRPTSSAVSYSPITSSASYSNVTPLTSSMDVPVYTGPDITLP-PTSVMEIYSP 419
DB 361 VPSRPTSSAVSYSPITSSASYSNVTPLTSSMDVPVYTGPDITLP-PTSVMEIYSP 419
QY 420 APASNOYICIGHGYHLYLPLLYFPKRRKRVYFPFADGVAA 461
DB 420 APASNOYICIGHGYHLYLPLLYFPKRRKRVYFPFADGVAA 461

```

RESULT 2

```

VL2_HPVA5 STANDARD: PRT: 463 AA.
AC P36761;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Minor capsid protein L2.
GN L2.
OS Human papillomavirus type 45.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10593;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9426501; PubMed=8205638;
RA "Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
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CC EMBL: X74479; CAAS2577.1; -.
DR PIR: S36565;
DR InterPro: IPR000784; Late_L2.
DR Pfam: PF00513; late_protein_L2; 1.
KW Coat protein; Late protein.
SQ SEQUENCE 463 AA; 49769 MW; 9BD69C97A9D005C6 CRC64;

```

```

Query Match 82.0%; Score 1973; DB 1; Length 463;
Best Local Similarity 81.7%; Pred. No. 4,1e-114;
Matches 379; Conservative 33; Mismatches 48; Indels 4; Gaps 3;

```

```

QY 1 MVSHRAARRKASVTDLYKTKQSGTSPDVNVNVEGTTLADKILQWSSLGIFLGAGIG 60
DB 1 MVSHRAARRKASVTDLYKTKQSGTSPDVNVNVEGTTLADKILQWSSLGIFLGAGIG 60
QY 61 TGSSTGRTGYIPLGKSNVVDVGPTRPVVIEPVGTPDSITVLVEDSSVVASGAPVP 120
DB 61 TGSSTGRTGYIPLGKSNVVDVGPTRPVVIEPVGTPDSITVLVEDSSVVASGAPVP 120
QY 121 TFGTSGFDITSACTTPPAVDITPSSTSVSIITNTNPAFSDPSTIEVQTEVSGNV 180
DB 121 TFGTSGFDITSACTTPPAVDITPSSTSVSIITNTNPAFSDPSTIEVQTEVSGNV 180
QY 181 FVGPTSGTHGEIEPILOTFASSSGTGEEPISTPLPYRRVAGPRLTSRAYQOVSANPE 240
DB 181 FVGPTSGTHGEIEPILOTFASSSGTGEEPISTPLPYRRVAGPRLTSRAYQOVSANPE 240

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```

QY 241 FLTRPSSLLTYDNPAFEVDTTLTFEPNSNVPDSDFMIDILHRPALTSRRGTVAFSRLG 300
DB 241 FLTRPSSLLTYDNPAFEVDTTLTFEPNSNVPDSDFMIDILHRPALTSRRGTVAFSRLG 300
QY 301 ORATMFRTSSGQIOGARVHFYHDISPIAPSPYEILOPLVSAITEDGLFADDDIDPAMP 360
DB 301 ORATMFRTSSGQIOGARVHFYHDISPIAPSPYEILOPLVSAITEDGLFADDDIDPAMP 360
QY 361 VPSRPTSSAVSYSPITSSASYSNVTPLTSSMDVPVYTGPDITLP-PTSVMEIYSP 417
DB 361 VPSRPTSSAVSYSPITSSASYSNVTPLTSSMDVPVYTGPDITLP-PTSVMEIYSP 417
QY 418 PTASASTOYICIGHGYHLYLPLLYFPKRRKRVYFPFADGVAA 461
DB 418 PTASASTOYICIGHGYHLYLPLLYFPKRRKRVYFPFADGVAA 461

```

RESULT 3

```

VL2_HPVM STANDARD: PRT: 469 AA.
AC P27965;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Minor capsid protein L2.
GN L2.
OS Human papillomavirus type ME180.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374616; PubMed=1716694;
RA Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;
RT "Characterization of a novel human papillomavirus DNA in the cervical
RL J. Virol. 65:5564-5568(1991).
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CC EMBL: M73258; AAF14009.1; -.
DR PIR: A40509; P2M1PR.
DR InterPro: IPR000784; Late_L2.
DR Pfam: PF00513; late_protein_L2; 1.
KW Coat protein; Late protein.
SQ SEQUENCE 469 AA; 50008 MW; F82425277C9FE9B1 CRC64;

```

```

Query Match 71.4%; Score 1716; DB 1; Length 469;
Best Local Similarity 70.1%; Pred. No. 2.4e-98;
Matches 329; Conservative 62; Mismatches 68; Indels 10; Gaps 4;

```

```

QY 1 MVSHRAARRKASVTDLYKTKQSGTSPDVNVNVEGTTLADKILQWSSLGIFLGAGIG 60
DB 1 MVSHRAARRKASVTDLYKTKQSGTSPDVNVNVEGTTLADKILQWSSLGIFLGAGIG 60
QY 61 TGSSTGRTGYIPLGKSNVVDVGPTRPVVIEPVGTPDSITVLVEDSSVVASGAPVP 120
DB 61 TGSSTGRTGYIPLGKSNVVDVGPTRPVVIEPVGTPDSITVLVEDSSVVASGAPVP 120
QY 121 TFGTSGFDITSACTTPPAVDITPSSTSVSIITNTNPAFSDPSTIEVQTEVSGNV 180
DB 121 TFGTSGFDITSACTTPPAVDITPSSTSVSIITNTNPAFSDPSTIEVQTEVSGNV 180
QY 181 FVGPTSGTHGEIEPILOTFASSSGTGEEPISTPLPYRRVAGPRLTSRAYQOVSANPE 240
DB 181 FVGPTSGTHGEIEPILOTFASSSGTGEEPISTPLPYRRVAGPRLTSRAYQOVSANPE 240

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Db      241 EYTHSSFEYENPAFEPPDTLLTLEADIAADPPDLVLRHRLPRLSRKGTVRSRIG 300
Qy      301 ORATMETRSQTIGARVHFYHDISPAPSEYELQPLVSA---TEDNGLFIYAD-DID 356
Db      301 KATVWTRGTQIGAOVHYHDISSLAPE-ESIELQPLVHAPSPASDALLFIYADVNN 359
Qy      357 PAMPFSPRTTSSAVTYS---PTISSASS--YSNVYPLTSSMDVPYTGPDITLPT 410
Db      360 TYLDIAFNNTKDSG--TTYNTGSLPSVASASTKRYANTLIPFSTSNMMPVNTGPDIALPST 418
Qy      411 SWMPVSPAPASTOY-IGIHGTHYLLMPLYYFIPKRRKRVYFFADGFVA 460
Db      419 TPQLPLVPSGPIIDTYAITIGSNYYLPLFLFKRRKRIYFFSDGYA 469

RESULT 6
V12_HPV29          STANDARD:      PRT: 473 AA.
AC      P50800:
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      01-OCT-1996 (Rel. 34, Last annotation update)
DE      Minor capsid protein L2.
GN      L2.
OS      Human papillomavirus type 29.
OC      Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      Papillomavirus.
OX      NCBI_TaxID=37112;
RN      [1]
RP      SEQUENCE FROM N.A.
RL      Delius H.;
RT      Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
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DR      EMBL; U31784; AAA9434.1; -.
DR      InterPro: IPR000784; Late_L2.
DR      Pfam: PF00513; late_protein_L2; 1.
KW      Coat protein; Late protein.
SQ      SEQUENCE 473 AA; 50631 MW; 70373961C694DB99 CRC64;

Query Match          64.4%; Score 1550; DB 1; Length 473;
Best Local Similarity 63.9%; Pred. No. 3.7e-88;
Matches 304; Conservative 67; Mismatches 85; Indels 20; Gaps 10;

Qy      1 MWSHRAARRKRASTVDLYKTKQSGTCDPVVNVKVEGTTLADKILQWSSLGIFLGIG 60
Db      1 MVAHRAARRKRASTATLYKTKCKAGTCTPPVDPKVEGTTLADRILOWSSLGIVLGIG 60
Qy      61 TSGSGGTGTGYIPLGGRNTVVDVG--PTRPPVYIEPVPTDPSYTLIEDSSVVTSGAPR 119
Db      61 TSGSGGTGTGYIPVGRGTGVVDVSIPTRPVYIEPVGPSPDSYTLIESSVINSAGTI 120
Qy      120 PTFGTSGFDITSGATTPPAVLDTIPSSSTVISSTNTNPAFSPSIIIEYPOGGEVGN 179
Db      121 PTFGTSGFELTSSATTPPAVLDTIPADNVITSTNNNPLFTFPPSLIETPQIGETSGR 180
Qy      180 VFGVPTISGTHGYEIRIPLQTFPASSGTGEPISSPPLPVRVAVAGPRLYSRAVVOOVSVNP 239
Db      181 VLVGPTISGVHGYEIRIPMDTFATSGTGLEPISSTPVPVSRVAGPRLYGKALTYRVADP 240
Qy      240 EFLRPSSLLTYDNPAPFEPVDTTLFE--PRSNVPDSDPMDIIRLHAPALTSRRGYRF 296
Db      241 AFLTPQSSFEVTFEDNPVDEDEETIIIFERPSPGTVPDPDMDIYLRHAPALTSRRGYRF 300
Qy      297 SRLGQATMTFTRSGTQIGARVHFYHDISPAPSEYELQPLVSA---SATEDNGLFEDIYA- 352

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Db      301 SVVQKFSMRKTRSGTNIGARVHYHDLSPILPT-EDIELEPLLPADPTAEESLVDIYAD 359
Qy      353 -DDIPAMPVSPRPPTS-----SAVSYPSTISSASSSVYVPLTSSMDVPYTGPDITL 407
Db      360 VDEADMAFTGGGRGATTYGRTTPSVFSTLS--TRIGNVYTLPTWSPVDVPLHTGPDITL 417
Qy      408 PPTSWMPVIVSPAPA-STOYIGIHGTHYLLMPLYYFIPK--RKRPVFFADGFVA 460
Db      418 PSSAQMPFV-PVAPADTFHYHYIDGADVFLMFVPTPVSRRKRRKRLSFLADGFVA 472

RESULT 7
V12_HPV10          STANDARD:      PRT: 470 AA.
AC      P36747;
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      01-OCT-1996 (Rel. 34, Last annotation update)
DE      Minor capsid protein L2.
GN      L2.
OS      Human papillomavirus type 10.
OC      Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      Papillomavirus.
OX      NCBI_TaxID=10603;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE-94265501; PubMed-8205838;
RA      Delius H., Hofmann B.;
RT      "Primer-directed sequencing of human papillomavirus types.";
RL      Curr. Top. Microbiol. Immunol. 186:13-31(1994).
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X74465; CAA52493.1; -.
DR      PIR: S36536; S36536.
DR      InterPro: IPR000784; Late_L2.
DR      Pfam: PF00513; late_protein_L2; 1.
KW      Coat protein; Late protein.
SQ      SEQUENCE 470 AA; 50583 MW; 056EB847259436E6 CRC64;

Query Match          63.7%; Score 1532.5; DB 1; Length 470;
Best Local Similarity 63.9%; Pred. No. 4.3e-87;
Matches 301; Conservative 69; Mismatches 88; Indels 13; Gaps 9;

Qy      1 MWSHRAARRKRASTVDLYKTKQSGTCDPVVNVKVEGTTLADKILQWSSLGIFLGIG 60
Db      1 MVAQARARRKRASTATLYKTKCASGTCTPPVDPKVEGTTLADRILOWSSLGIVLGIG 60
Qy      61 TSGSGGTGTGYIPLGGRNTVVDVG--PTRPPVYIEPVPTDPSYTLIEDSSVVTSGAPR 119
Db      61 TSGSGGTGTGYIPSTRGTGVVDVSVPARPVYIEPVGPSPDSYTLNLEDSSINSGSTI 120
Qy      120 PTFGTSGFDITSGATTPPAVLDTIPSSSTVISSTNTNPAFSPSIIIEYPOGGEVGN 179
Db      121 PTFSTSGFEVYTSATTPPAVLDTIPASENVYISSTNTNPAFTFPPSLIIEYPOGGEVSGH 180
Qy      180 VFGVPTISGTHGYEIRIPLQTFPASSGTGEPISSPPLPVRVAVAGPRLYSRAVVOOVSVNP 239
Db      181 ILISPTAGTHGYEIRIPMDTFASSGTGEPISSTPVPVSVSLAGPRLYSRANTQYKSDP 240
Qy      240 EFLRPSSLLTYDNPAPFEPVDTTLFE--PRSNVPDSDPMDIIRLHAPALTSRRGYRF 296
Db      241 AFLRPSSLLTFDNPVFEDEDEETIIIFERPSPGTVPDPDMDIYLRHAPALTSRRGYRF 300
Qy      297 SRLGQATMTFTRSGTQIGARVHFYHDISPAPSEYELQPLVSA---SATEDNGLFEDIYA--DD 354

```

DB 301 SRLGQFMSRTRSGKIGARVHYQDLSPAPI-EDIEMEPILAPASDITVIFADVDD 359

QY 355 IIPAMPVPSRPTSS-AVSTYSPFTSSASS-YSNATVPLTSSMDVPVYTGPDITLPTSY 412

DB 360 GVAFAFEGYRSTQSGYNTTSLSTSKYGNVPIPFVS PVDVTLHFGPDIVLPTSAQ 419

QY 413 WPIVSTAPA-SVOYIGHGHYLMPLYFIP-KKKRVPEFADGFAA 460

DB 420 WPIV-PLSPADTHHYIDGDFYIMPVTFHFSRRRRRRVSYEFADGTLA 469

RESULT 8

VL2_HPV30 STANDARD; PRT; 463 AA.

AC P36756;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Minor capsid protein L2.

GN L2.

OS Human papillomavirus type 30.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10611;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94265501; PubMed=8205838;

RA Delius H., Hofmann B.;

RT "Primer-directed sequencing of human papillomavirus types.";

RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).

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CC -----

DR EMBL; X74474; CAA52547.1; -

DR PIR; S36507; S36507.

DR InterPro; IPR000784; Late_L2.

DR Pfam; PF00513; late_protein_L2; 1.

KW Coat protein; late protein.

SQ SEQUENCE 463 AA; 49903 MW; 9B5B526107F2B072 CRC64;

Query Match 63.6%; Score 1530; DB 1; Length 463;

Best local Similarity 63.2%; Pred. No. 6, 1e-87;

Matches 295; Conservative 68; Mismatches 94; Indels 10; Gaps 8;

QY 1 MSHRAARRRRASVTDLYTKCKSGTCPSDVNKNVKGTTLADKILQWSSLGIFLAGIGIG 60

DB 1 MVAHRRARRRRRASATQYQCKQAGTSPDVINKIEHTTLADKILQWSSLGIFLAGIGIG 60

QY 61 TSGGTGRCGYTILPLGSRNTVVDVGPTRPVVIEPVGPDPSIVTLIEDSSVYTGAPRP 120

DB 61 TSGGTGRCGYTILPLGSRNTVVDVGPTRPVVIEPVGPDPSIVTLIEDSSVYTGAPRP 120

QY 121 TFGTSGFDITSAAGTTTAVLDITPSTSVISSTNTFNTPAFSDPSIIIEVPGTGEVGNV 180

DB 121 NFGTSGFEVTSSTTTTAVLDITPSTSVISSTNTFNTPAFSDPSIIIEVPGTGEVGNV 180

QY 181 FVGTPTSGHGYEILPLQTFPAGSGTEPISTPLTVRRVAGPRLYSRAVOOVYANPE 240

DB 181 LVSTPTSGVHYEILPMQTFAGVGTETPISSTPIGLRIAPRLYKQAFQVKTDP 240

QY 241 FLTRPSLLTYNDNAPAPVPVDTTLTFRSRNVPSDPMDDIIRLRPALTSRGRVRSRLG 300

DB 241 FLTRPETLLTYNDNAPVEDADTTLTFRSPGVAPDPDLIALHRAFTTTRGGVRSRLG 300

QY 301 QRAFMFTSGTQIGARVHYNDISIPASPEYTELOPLVSATED--GLFDIYADDIDP 359

DB 301 TKATMTRSGKQIGARVHYNDISIPASPEYTELOPLVSATED--GLFDIYADDIDP 359

QY 360 PVSRSPT--TSSAVSYSPFTSSASSYSNATVPLTSSMDVPVYTGPDITL--PISVWPI 415

DB 359 PVSSHLSIAPSRSLPTNTVPLSFSQTNVTIPLGKWDVPIVSGDVIPLPTPT--WP- 416

QY 416 VSPFAPASVOY-IGINGHGHYLMPLYFIPKKRRKRPYFPAADGFAA 461

DB 417 YAPADPDTTHDVYIGHSTFALMPVYFLRRRRRRKHVYFLADGVAA 463

RESULT 9

VL2_HPV53 STANDARD; PRT; 463 AA.

AC P36764;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Minor capsid protein L2.

GN L2.

OS Human papillomavirus type 53.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10619;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94265501; PubMed=8205838;

RA Delius H., Hofmann B.;

RT "Primer-directed sequencing of human papillomavirus types.";

RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).

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DR EMBL; X74482; CAA52594.1; -

DR PIR; S36530; S36530.

DR InterPro; IPR000784; Late_L2.

DR Pfam; PF00513; late_protein_L2; 1.

KW Coat protein; late protein.

SQ SEQUENCE 463 AA; 50118 MW; F065B5E7A518EA3E CRC64;

Query Match 63.6%; Score 1529; DB 1; Length 463;

Best local Similarity 63.2%; Pred. No. 7e-87;

Matches 297; Conservative 63; Mismatches 94; Indels 16; Gaps 9;

QY 1 MSHRAARRRRASVTDLYTKCKSGTCPSDVNKNVKGTTLADKILQWSSLGIFLAGIGIG 60

DB 1 MVAHRRARRRRRASATQYQCKQAGTSPDVINKIEHTTLADKILQWSSLGIFLAGIGIG 60

QY 61 TSGGTGRCGYTILPLGSRNTVVDVGPTRPVVIEPVGPDPSIVTLIEDSSVYTGAPRP 120

DB 61 TSGGTGRCGYTILPLGSRNTVVDVGPTRPVVIEPVGPDPSIVTLIEDSSVYTGAPRP 120

QY 121 TFGTSGFDITSAAGTTTAVLDITPSTSVISSTNTFNTPAFSDPSIIIEVPGTGEVGNV 180

DB 121 NFGTSGFEVTSSTTTTAVLDITPSTSVISSTNTFNTPAFSDPSIIIEVPGTGEVGNV 180

QY 181 FVGTPTSGHGYEILPLQTFPAGSGTEPISTPLTVRRVAGPRLYSRAVOOVYANPE 240

DB 181 LVSTPTSGVHYEILPMQTFAGVGTETPISSTPIGLRIAPRLYKQAFQVKTDP 240

QY 241 FLTRPSLLTYNDNAPAPVPVDTTLTFRSRNVPSDPMDDIIRLRPALTSRGRVRSRLG 300

DB 241 FLTRPETLLTYNDNAPVEDADTTLTFRSPGVAPDPDLIALHRAFTTTRGGVRSRLG 300

QY 301 QRAFMFTSGTQIGARVHYNDISIPASPEYTELOPLVSATEDN--GLFDIYADDIDP 357

DB 301 TKATMTRSGKQIGARVHYNDISIPASPEYTELOPLVSATEDN--GLFDIYADDIDP 357

DB 420 SAKMFPV-PLSPVDYTHVYIDGGDFYLMPTFFELPRRRRRKRVSTFLADGVA 472

RESULT 12

VL2_HPV56

STANDARD;

PRT;

464 AA.

AC 080960;

15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 36, Last sequence update)

15-JUL-1998 (Rel. 36, Last annotation update)

DE Minor capsid protein L2.

GN

OS Human papillomavirus type 66.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_Taxid=37119;

RN [1]

RP SEQUENCE FROM N.A.

RA Delius H.;

RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.

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CC

CC EMBL: U31794; AAA79504.1; -

DR InterPro: IPR000784; Late_L2.

DR Pfam: PF00513; Late_protein_L2; 1.

KW Coat protein; Late protein.

SQ SEQUENCE 464 AA; 49988 MW; 19C3D0FCE131FE2 CRC64;

Query Match

Best Local Similarity 62.1%; Score 1493.5; DB 1; Length 464;

Matches 291; Conservative 63; Mismatches 104; Indels 9; Gaps 8;

DB 1 MYSHRAARRKRAVTDLYKTCOSGCPDVKVKGVTTLADKILQWSSLGIFLGGIG 60

1 MAHRAIRRRKRAVTDLYKTCOSGCPDVKVKGVTTLADKILQWSSLGIFLGGIG 60

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

RESULT 13

VL2_HPV56

STANDARD;

PRT;

464 AA.

AC P36765;

01-JUN-1994 (Rel. 29, Created)

01-JUN-1994 (Rel. 29, Last sequence update)

01-OCT-1996 (Rel. 34, Last annotation update)

DE Minor capsid protein L2.

GN

OS Human papillomavirus type 56.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_Taxid=10596;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-9426501; Pubmed-8205838;

RA Delius H., Hofmann B.;

Primer-directed sequencing of human papillomavirus types.;

RL Curr. top. Microbiol. Immunol. 186:13-31(1994).

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CC

CC EMBL: X74483; CA52599.1; -

DR PIR: S36582; S36582.

DR InterPro: IPR000784; Late_L2.

DR Pfam: PF00513; Late_protein_L2; 1.

KW Coat protein; Late protein.

SQ SEQUENCE 464 AA; 49983 MW; 41B6687D5C8E7E21 CRC64;

Query Match

Best Local Similarity 61.8%; Score 1486.5; DB 1; Length 464;

Matches 284; Conservative 68; Mismatches 108; Indels 5; Gaps 4;

DB 1 MYSHRAARRKRAVTDLYKTCOSGCPDVKVKGVTTLADKILQWSSLGIFLGGIG 60

1 MAHRAIRRRKRAVTDLYKTCOSGCPDVKVKGVTTLADKILQWSSLGIFLGGIG 60

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

61 TSGSGGRTGYPLDGRSNTVDVGPTRPVVIEVPPTDPSIVTLIEDSVVTSGAPR 120

RESULT 14

```

VL2_HPV26          STANDARD:      PRT:      472 AA.
ID  VL2_HPV26
AC  P36754.
DT  01-JUN-1994 (Rel. 29, Created)
DT  01-JUN-1994 (Rel. 29, Last sequence update)
DT  01-OCT-1996 (Rel. 34, Last annotation update)
DE  Minor capsid protein L2.
GN  L2.
OS  Human papillomavirus type 26.
OC  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OX  Papillomavirus.
RN  NCBI_TaxID=31549;
RP  [1]
RX  MEDLINE=94265501; Pubmed=8205838;
RA  DeLius H., Hotmann B.;
RT  Primer-directed sequencing of human papillomavirus types.;
RL  Curr. Top. Microbiol. Immunol. 186:13-31(1994).
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CC  -----
DR  EMBL: X74472; CAA52534.1; -
DR  PIR: S36548; S36548.
DR  InterPro: IPR000784; Late_L2.
DR  Pfam: PF00513; late_protein_L2; 1.
KW  Coat protein; Late protein.
SQ  SEQUENCE 472 AA; 50613 MW; DA05C41B80FB6C50 CRC64;

Query Match      61.7%; Score 1483.5; DB 1; Length 472;
Best Local Similarity 60.8%; Pred. No. 4,4e-84;
Matches 287; Conservative 81; Mismatches 91; Indels 13; Gaps 10;

QY  1  MWSHRAARRKRAVTDLYKTKQSGTSPDVNVNVEGTTLADKILQWSSLGIFLGLGIG 60
DB  1  MVAIRARRRRKRASTIDLYKTKKAGTCCPDVYPRKESTAGTKLQWSSLGIFLGLGIG 60
QY  61  TGSCTGRTGYIPILGGSNT-VVDVGPTRPPVIEPVPDPSPITVTLIEDSSVYTSQAPR 119
DB  61  TGTSGGRTGYIPLGGGRRPVDVIGTPRPPIIEPVPDPSPITVTLIEDSSVYTSQAPR 120
QY  120  PTFGTGSGFDITSGITTPPAVLDTTPSTSVSISTNFTNPAFSDPSITIEVPQGEVSGN 179
DB  121  PTFSGGNGFELTSSATTPPAVLDTTPSAGTVHVTSTNQNPYLEPP-IDIPQAGEASGH 179
QY  180  VFTGPTSGTHGYEIPILQTFPAS-SGTGEPISTPLPYRRVAGPRLYSAYQOVSAN 238
DB  180  IFTTSTAGTHSYEIMEVFASNGTGLEISTPIPGIOKVAPRLYSAYQOVSAN 239
QY  239  PEFLTRPSLITVYNPAPFEPVDTLTFEPKSNV-PDSDFMDIILHAPALTSRGGYRFS 297
DB  240  PNFIGNSTFTVFNPAPEPDIETLTYAASSSTVAPDDFDIILHAPALTSRGGYRFS 299
QY  298  RLQGRATMFTRSQGIARVHFHYHDIAPSPPEY--IELOPLVSATEDNGS-LFDIYAD- 353
DB  300  RLQGRATMFTRSQGIARVHFHYHDIAPSPPEY--IELOPLVSATEDNGS-LFDIYADP 359
QY  354  DIDPAMVP--SRETTSAVSTYSPTISSA--SSYSNVTVPILTSMDVPVYTGPDITLPP 409
DB  360  DYPVSIHTPRKMSYPTLPPPRKASNVSSSTNTSTNTVTPPLSTSELPYSGSDIYTP 419
QY  410  TS-VMPVSPAPASTQYIGIHGHYVLYLPLLYPILPKRRKRVPPFADGEVA 460
DB  420  SSPWPELPPRPPTTNLPAIVYHGDNVYLYMPLYIILHRRKRMPIFFSDGEVA 471

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ID  VL2_HPV51          STANDARD:      PRT:      468 AA.
AC  P26539;
DT  01-AUG-1992 (Rel. 23, Created)
DT  01-AUG-1992 (Rel. 23, Last sequence update)
DT  01-OCT-1996 (Rel. 34, Last annotation update)
DE  Minor capsid protein L2.
GN  L2.
OS  Human papillomavirus type 51.
OC  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OX  Papillomavirus.
RN  NCBI_TaxID=10595;
RP  [1]
RX  MEDLINE=91303675; Pubmed=1649326;
RA  Lungu O., Crum C.P., Silverstein S.J.;
RT  Biologic properties and nucleotide sequence analysis of human
RL  papillomavirus type 51.;
J. Virol. 65:4216-4225(1991).
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CC  -----
DR  EMBL: M62877; -; NOT_ANNOTATED_CDS.
DR  PIR: H40415; P2ML51.
DR  InterPro: IPR000784; Late_L2.
DR  Pfam: PF00513; late_protein_L2; 1.
KW  Coat protein; Late protein.
SQ  SEQUENCE 468 AA; 50720 MW; B5BAC02A12712743 CRC64;

Query Match      61.0%; Score 1466.5; DB 1; Length 468;
Best Local Similarity 61.1%; Pred. No. 4,8e-83;
Matches 288; Conservative 78; Mismatches 90; Indels 15; Gaps 10;

QY  1  MWSHRAARRKRAVTDLYKTKQSGTSPDVNVNVEGTTLADKILQWSSLGIFLGLGIG 60
DB  1  MVAIRARRRRKRAVTDLYKTKKAGTCCPDVYPRKESTAGTKLQWSSLGIFLGLGIG 60
QY  61  TGSCTGRTGYIPILGGSNT-VVDVGPTRPPVIEPVPDPSPITVTLIEDSSVYTSQAPR 119
DB  61  TGTSGGRTGYIPLGGGRRPVDVIGTPRPPIIEPVPDPSPITVTLIEDSSVYTSQAPR 120
QY  120  PTFGTGSGFDITSGITTPPAVLDTTPSTSVSISTNFTNPAFSDPSITIEVPQGEVSGN 179
DB  121  PTFGTGSGFELTSSSTTPPAVLDTTPSAGTVHVTSTNQNPYLEPP-IDIPQAGEASGH 179
QY  180  VFTGPTSGTHGYEIPILQTFPAS-SGTGEPISTPLPYRRVAGPRLYSAYQOVSAN 238
DB  180  IYLVHSGTHGYEIMEVFASNGTGLEISTPIPGIOKVAPRLYSAYQOVSAN 239
QY  239  PEFLTRPSLITVYNPAPFEPVDTLTFEPKSNV-PDSDFMDIILHAPALTSRGGYRFS 297
DB  240  PNFIGNSTFTVFNPAPEPDIETLTYAASSSTVAPDDFDIILHAPALTSRGGYRFS 299
QY  298  RLQGRATMFTRSQGIARVHFHYHDIAPSPPEYIELOPLVSATEDNGS-LFDIYADIDP 357
DB  300  RLQGRATMFTRSQGIARVHFHYHDIAPSPPEYIELOPLVSATEDNGS-LFDIYADIDP 356
QY  358  A-----MPVSRPTTSAVSTYSPTISSA--SSYSNVTVPILTSMDVPVYTGPDITLPP 410
DB  357  AETGFIQPTHTTPSHSLSRQLPSLSSMSSTVANTIPFTSPSTVSPHITGPDVYLP 416
QY  411  TS-VMPVSPAPASTQYIGIHGHYVLYLPLLYPILPKRRKRVPPFADGEVA 460
DB  417  PTWVPVPHNSIDTKHSIVILGIDYLYMPLYIILHRRKRMPIFFSDGEVA 467

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Db      61 TGGGTGRTGYIPLGRTNTIVDSAPKPVVIEVGPDPDSIVTLVEDSSVITSGAPAP 120
Qy      121 TFTGTSGFDITSAGTTTDAVIDITPSSVSISTNTFTNPAFSDSIIIEVPQTGEVSGNV 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 TFTGTSGFEISSTTTPAVLIDITPTS--SVQISSSSFNPAFTDPSVIEVPQTGEISGNI 179
Qy      181 FVGTSTGCHGEEELPLOTFASSGCEPISSTPLPYRRVAGPRLYSRAVQVSVANPE 240
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      180 LISTSTSAHGEEELPMQTFNEGTEGLEPISSTPNPYRRVAGPRLYSRAVQVSVANPD 239
Qy      241 FLTRPSSLTITDNPFAPEVDITLTFEPRSNDPDSFMDIIRLHRALTSRSGTVAFSRIG 300
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      240 FLTRSTFTYDNPVADPIDTLTTFDPSSSEVDPDPFMDIIRLHRALTSRSGTVAFSRIG 299
Qy      301 ORATMFTSRGQIOIGARVHFHYHDISPAPSEYIELQPLV---ATEDNGLEDIYADIDP 357
Db      300 ORATMFTSRGQIOIGARVHFHYHDISPAPSEYIELQPLV---ATEDNGLEDIYADIDP 356
Qy      358 AMPVPSRPTT---SSAVSYSPITSSASVSNTVPLTSSMDVYVYTGPDITLTPPTS-V 412
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      357 A-PISTANTATFTPKSSPQSLTRSSASTSNVPLATADVNTGPDITLTPNTIV 415
Qy      413 WPVSPAPASTQYIGIHGTHYLLPLLYFIKPKRRVYFPADGEVA 460
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      416 EPTVSTPTFTTQISINIGTNTFLMPITYFLPKRRKRVYFPPTDGSMA 463

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RESULT 2

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O9WHG6 PRELIMINARY; PRT; 467 AA.
ID AC O9WHG6
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative minor capsid protein L2.
GN L2.
OS Human papillomavirus candid HPV85.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=151757;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20047972; PubMed=10580054;
RA Chow V.T.K., Leong W.F.;
RT "Complete nucleotide sequence, genomic organization and phylogenetic
analysis of a novel genital human papillomavirus type, HLT7474-S."
RL J. Gen. Virol. 80:2923-2929(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Chow V.T.K., Leong W.F.;
RL Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131950; AAD24187.1; -.
DR InterPro; IPR000784; Late_L2.
DR Pfam; PF00513; late_protein_L2; 1.
SQ SEQUENCE 467 AA; 50394 MW; 773F18A2525F5235 CRC64;

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Query Match 73.8%; Score 1774; DB 12; Length 467;
 Best Local Similarity 72.4%; Pred. No. 5.9e-111;
 Matches 343; Conservative 51; Mismatches 58; Indels 22; Gaps 7;

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Qy      1 MWSHRAARRKRASTVDLYKTKQSGTSPDVYNNKVEGTTTLADKILLQSSLGIFLGIGIG 60
Db      1 MWSHRAARRKRASTVDLYKTKQSGTSPDVYNNKVEGTTTLADKILLQSSLGIFLGIGIG 60
Qy      61 TGGGTGRTGYIPLGGRNTVVDVGPTRPPVPIEVPVGPDPDSIVTLIEDSSVYTSAGAPR 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 TGGGTGRTGYIPLGGRNTVVDVGPTRPPVPIEVPVGPDPDSIVTLIEDSSVYTSAGAPR 120
Qy      121 TFTGTSGFDITSAGTTTDAVIDITPSSVSISTNTFTNPAFSDSIIIEVPQTGEVSGNV 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 TFTGTSGFEISSTTTPAVLIDITPTS--SVQISSSSFNPAFTDPSVIEVPQTGEISGNI 180
Qy      181 FVGTSTGCHGEEELPLOTFASSGCEPISSTPLPYRRVAGPRLYSRAVQVSVANPE 240

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Db      181 FITPSTGCHGEEELPMHTFAQTQCRTEPISSTPLPYRRVAGPRLYSQAQVQKVTMSD 240
Qy      241 FLTRPSSLTITDNPFAPEVDITLTFEPRSNDPDSFMDIIRLHRALTSRSGTVAFSRIG 300
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 FISRSSTLVTTNPAVEPIDTLTTFSPDQVVPDPDPFMDIIRLHRALTSRSGTVAFSRIG 300
Qy      301 ORATMFTSRGQIOIGARVHFHYHDISPAPSEYIELQPLV---SATED-NGLEDIYAD-DI 355
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301 KLTFTSRGQIOIGARVHFHYHDISPISHIGSEIEMQPLLPDAVA7ADTNGLEDIYADTDI 360
Qy      356 DPAMVPSR-----PTSSASVSISTPSSAS--YANVYVPLTSSMDVYVYTGPDITL 407
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      361 DNAMALYDRNISDVQTPTS-----TSSVSRSYNTTPIATSDVYVHTGPDITL 412
Qy      408 PPT-SVMPVSPAPASTQYIGIHGTHYLLPLLYFIKPKRRVYFPADGEVA 460
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      413 PTTIPQWNTIVPLPNTNHSVLOGTNTYLLPNNTYFIKPKRRVYFPLTDEGVA 466

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RESULT 3

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O99324 PRELIMINARY; PRT; 473 AA.
ID AC O99324
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Putative minor capsid protein L2.
GN L2.
OS Human papillomavirus type 82.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=129724;
RN [1]
RP SEQUENCE FROM N.A.
RA Terai M., Burk R.D.;
RT "Cervical HPV's in Evolution; Genomic Sequence of IS39/AE2, a Subtype
of Oncogenic HPV 82 (W13B).";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF293961; AAK28455.1; -.
DR InterPro; IPR000784; Late_L2.
DR Pfam; PF00513; late_protein_L2; 1.
SQ SEQUENCE 473 AA; 51047 MW; 3E31D2870668F03 CRC64;

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Query Match 65.0%; Score 1563; DB 12; Length 473;
 Best Local Similarity 62.8%; Pred. No. 8.3e-97;
 Matches 297; Conservative 75; Mismatches 87; Indels 14; Gaps 7;

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Qy      1 MWSHRAARRKRASTVDLYKTKQSGTSPDVYNNKVEGTTTLADKILLQSSLGIFLGIGIG 60
Db      1 MWSHRAARRKRASTVQLXSTCKAAGTCAVDIAPKVEGTTTLADKILLQSSLGIFLGIGIG 60
Qy      61 TGGGTGRTGYIPLGGRNT-VVDVGPTRPPVPIEVPVGPDPDSIVTLIEDSSVYTSAGAPR 119
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 TGGGTGRTGYIPLGGRNTPGVVDIAPARPPIIIEPAVATPDSIVNLVEDSSITNSGSTI 120
Qy      120 PFTGTSGFDITSAGTTTDAVIDITPSSVSISTNTFTNPAFSDSIIIEVPQTGEVSGNV 179
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 PFTGTGDFEITSSTTTPAVLIDITPSTGTVRSTNIENLPIEPPTEAPQSGEVSCH 180
Qy      180 VFGVTPSTGCHGEEELPLOTFASS-GIGEPISSSTPLPYRRVAGPRLYSRAVQVSVAN 238
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 IFSTPTSGTCHGEEELPMETVFAVSNGEQPISSTPTPGVARIAPRLYSRAVQVYKVN 240
Qy      239 PEFLTRPSSLTITDNPFAPEVDITLTFEPRSNDPDSFMDIIRLHRALTSRSGTVAFS 297
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 PDFLSRPSFVTFNPAPFIDASISGEPTVAPDPDFDIIRLHRALTSRSGTVAFS 300
Qy      298 RLQGRATMFTSRGQIOIGARVHFHYHDISPAPSEYIELQPLVSAATEDNGLEDIYAD---- 353
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301 RLQGRATMFTSRGQIOIGARVHFHYHDISPAPSEYIELQPLVSAATEDNGLEDIYADDEA 359
Qy      354 ---DIDPAMPVPSRPTTSSAVSYSPITSS--ASSYSNVTVPLTSSMDVYVYTGPDITLP 408

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Db      | 360 EINGEFTPTTTPALRRSSYSPLSTQDLPSSSVSSSYANVTTPSTTYHPVHPGPPVLP 419
Oy      | 409 PT-SWAPIVSPTAPASTOYIGHGHYVLYPLFYPPKRRKRPVYAGGFA 460
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      | 420 TSPYVFPFPHITSIDQHAIVLOGSDYIMPTTYLLKRRKRRIYFADGFA 472

RESULT 4
056950  PRELIMINARY; PRT; 519 AA.
ID      | 056950
AC      | 056950
DT      | 01-JUN-1998 (TReMBLrel. 06, Created)
DT      | 01-JUN-1998 (TReMBLrel. 06, last sequence update)
DE      | 01-DEC-2001 (TReMBLrel. 19, last annotation update)
GN      | L2 protein.
OS      | Human papillomavirus type 77.
OC      | Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      | Papillomavirus.
OX      | NCBI_TaxID=69986;
RN      | [1]
RP      | SEQUENCE FROM N.A.
RX      | MEDLINE=98118461; PubMed=9454709;
RA      | Dellus H., Saegling B., Bergmann K., Shamanin V., de Villiers E.M.;
RT      | "The genomes of three of four novel HPV types, defined by differences
RT      | of their L1 genes, show high conservation of the E7 gene and the
RT      | URR.";
RL      | Virology 240:359-365(1998).
DR      | EMBL: Y15175; CA75467.1; -
DR      | InterPro: IPR000784; Late_L2.
DR      | Pfam: PF00513; Late-protein_L2; 1.
SQ      | SEQUENCE 519 AA; 56079 MW; 888F1407D9C114D0 CRC64;

Query Match
Best Local Similarity 63.7%; Score 1533; DB 12; Length 519;
Matches 302; Conservative 70; Mismatches 85; Indels 18; Gaps 10;

Oy      | 1 MVSHRAARRKASVTDLYKTKOSGTCPSDVVNVKVGTTLADKILQWSSIGIFLGIGIG 60
        | ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      | 47 MVAHRARRRRKRSATLKYCKAKGCPDVPJPKVGGTTLADRIILQWGLGIVYLGGLGIG 106
Oy      | 61 TSSGTGRTGYIPLGSRNTVDVG-PTRPVYIEVGPDPDSIVTLIEDSSVYTGAPR 119
        | ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      | 107 TGTGTGGRTGYIPGIRPVTVDVSVPTRPVYIEVGPDPDSIVTLIEDSSVYIDGASG 166
Oy      | 120 PFTGSGFDITSAGTTPAVLDITPSSSVSISTNFNPAPSDSIIEVPTGEGSN 179
        | ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      | 167 PFTGSGFEITSSATTPAVLDITPAGDTVYVTSINFTNPLTIESLVEVPQTGEISGH 226
Oy      | 180 VEVGPTSGTHGEELIPLQTFASSSGTEEPISSTPLPTVRRVAGPRLYSRAVOQVSANP 239
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      | 227 LVTSTATSGHGEELIPMDTFANSGTSEPISTPVGYSRVAGPRLYGAMQVAVPDP 286
Oy      | 240 EELTRSSSLTYDNPAAFEVDITLTPF---PNSNVDSDPMDIIRLHRPALISRRGVTF 296
        | ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      | 287 AFLSRSSSVTEPNVYDPGDEETIIFERSPGTRVYDPFLDIYRLHRPALTSRRGTVR 346
Oy      | 297 SRLGQATMETRSGTIGARVHFYHDISPIAPSEYIELOPIV-----SATEDGGLDPIYA 352
        | ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      | 347 SRKQGFASKRTNSGIGARVHYHDLSPITHT-EDIELEPLLPDADSADSDS-LTDVYA 404
Oy      | 353 --DDIDPAMPVPSRPPTSSAVSYSPGISASS--YSNVTVPLTSSMDVVPVYGPDTLP 408
        | ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      | 405 DVDDADVAFTNSRNLTFSGGRASSLPSALSTKIGNVTIPIISPVDVILHMGPDVLP 464
Oy      | 409 PYSWPIVSPFLAPA-STOYIGHGHYVLYPLFYIPKK--RRVPYFADGFA 460
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      | 465 SSQWMPFV--PVLPADTTHYVYIDGNGFIYLPVTFVSRRKRRRLISFFADGFA 518

RESULT 5
08JUN96

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ID      | 08JUN96
AC      | 08JUN96;
DT      | 01-OCT-2002 (TReMBLrel. 22, Created)
DT      | 01-OCT-2002 (TReMBLrel. 22, last sequence update)
DE      | 01-MAR-2003 (TReMBLrel. 23, last annotation update)
GN      | Putative minor capsid protein L2.
OS      | Human papillomavirus type 90.
OC      | Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      | Papillomavirus.
OX      | NCBI_TaxID=202251;
RN      | [1]
RP      | SEQUENCE FROM N.A.
RX      | MEDLINE=22079881; PubMed=12085327;
RA      | Terai M., Burk R.D.;
RT      | "Identification and Characterization of 3 Novel Genital Human
RT      | Papillomaviruses by Overlapping Polymerase Chain Reaction: candHPV89,
RT      | candHPV90, and candHPV91.";
RL      | J. Infect. Dis. 185:1794-1797(2002).
RN      | [2]
RP      | SEQUENCE FROM N.A.
RA      | Burk R.D., Terai M.;
RL      | Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR      | EMBL: AY057438; AYL14209.1; -
DR      | InterPro: IPR000784; Late_L2.
DR      | Pfam: PF00513; Late-protein_L2; 1.
SQ      | SEQUENCE 467 AA; 49577 MW; 9BFC3FE24461D5C4 CRC64;

Query Match
Best Local Similarity 62.4%; Score 1507; DB 12; Length 467;
Matches 292; Conservative 70; Mismatches 94; Indels 12; Gaps 7;

Oy      | 4 HRAARRKASVTDLYKTKOSGTCPSDVVNVKVGTTLADKILQWSSIGIFLGIGIG 63
        | ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      | 2 HRSKRRKRSATLKYCKAKGCPDVPJPKVGGTTLADRIILQWGLGIVYLGGLGIG 61
Oy      | 64 GTGRTGYIPLGSRNTVDVG-PTRPVYIEVGPDPDSIVTLIEDSSVYTGAPR 122
        | ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      | 62 GTGRTGYIPGIRPVTVDVSGPAPRPVYIEVGPADPSIVTLIEDSSIIAGSPHPF 121
Oy      | 123 TGTSGFDITSAGTTPAVLDITPSSSVSISTNFNPAPSDSIIEVPTGEGSN 182
        | ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      | 122 TGTGGEVNTASTTPAVLDITPSSGNGVQSSSFTNPLETEPAIYEPDAGCVTGHVY 181
Oy      | 183 GPTSGTHGEELIPLQTFASSSGTEEPISSTPLPTVRRVAGPRLYSRAVOQVSANP 242
        | ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      | 182 STPTASHGHEELIPMDTFANSGTSEPISTPVGYSRVAGPRLYGAMQVAVPDP 241
Oy      | 243 TRPSSSLTYDNPAAFEVDITLTPF--SNVPSDSDPMDIIRLHRPALTSRRGVTF 301
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      | 242 SQEFLVTVYDNPVFEETILFEHPSIHQVDPDPLDIYALHRPALTARGVTRSLQ 301
Oy      | 302 RATMPTRSRGQIGARVHFYHDISPIAPSEYIELOPVAS TED--NGLPIYADDTDPAM 359
        | ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      | 302 RATLKTSGRGIGATVHFYQDLSPIAVDELMOPLVSPDPYDLSLYADTASVSR 361
Oy      | 360 P--VPSRPTSSAVSYSPGISASSVSNVTVPLTSSMDVVPVYGPDTLP 415
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      | 362 HRLTTPRPSTPLQASVYVSSALSSAASNTYVPLSTGLDIPVSGPDSALPSSHAWPV 421
Oy      | 416 VSPFLAPAST--OYIGHGHYVLYPLFYIPKKRRKRPVYFADGFA 461
        | ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      | 422 --PPAPGVVPGSVIVNGSYVYLLPLGLLPKRRKRPPYFADGNGVA 467

RESULT 6
09JUN96
AC      | 09JUN96;
DT      | 01-OCT-2000 (TReMBLrel. 15, Created)
DT      | 01-OCT-2000 (TReMBLrel. 15, last sequence update)
DE      | 01-OCT-2002 (TReMBLrel. 22, last annotation update)
GN      | DNA, complete genome.

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GN L2.
OS Human papillomavirus type 69.
OC Viruses; dsDNA viruses, no RNA stage: Papillomaviridae;
OC Papillomavirus.
NCBI_TaxID=37121;
RN [1]
RP SEQUENCE FROM N.A.
RA Matsukura T., Sato T.;
RM Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087389; PubMed=10618284;
RA Kato N., Sato T., Sato Y., Sugase M., Matsukura T.;
RT "Molecular cloning and nucleotide sequence analysis of a novel human papillomavirus (type 82) associated with vaginal intraepithelial neoplasia.";
RL Clin. Diagn. Lab. Immunol. 7:91-95(2000).
DR EMBL; AB027020; BAA90733.1; -
DR InterPro; IPR000784; Late_L2.
DR Pfam; PF00513; late_protein_L2; 1
SQ SEQUENCE 467 AA; 50054 MW; 78E32A50ECE9326 CRC64;

Query Match 62.2%; Score 1497; DB 12; Length 467;
Best Local Similarity 60.7%; Pred. No. 2,1e-92;
Matches 284; Conservative 81; Mismatches 93; Indels 10; Gaps 9;

OY 1 MWSHRAARRKASVTDLYKTKCKSGTCDVYNNKVEGTTLADKILQMSLGIPLGIGIG 60
DB 1 MVAAYASRRKASADLTKCKCACTCPDVIPKIEGSLADKILQMSGLGIFLGIGIG 60
OY 61 TGSAGGRTGTYPLGGRSN-TVVDYGPTRPVYIEPPTDPTSTLTLEDSSVYTSAPR 119
DB 61 TGTGTGGRTGTYPLGGRSPSVVDIGPRTPLIEVGPTEPSTVTLVESSILQSGSPF 120
OY 120 PFTGTSGFDITSAGTTTAVLDITPSTSVSISTNTNPAFSDPILIEVPGCEVSGN 179
DB 121 PNFSGDGEVYTTSTTTPAVLDITPSPGVHTSTNQNPLYERP-VDIQSGEALGH 179
OY 180 VFGVPTSGTGHYEIPLOTFA--SGTGEPISTPLPTVRVAGPRLYSKAYQOVAN 238
DB 180 IFTSTGTGTHSYEIPMEVFAASMTSSGSKPISIPGIRRVAPRLYSKAYQOVKTD 239
OY 239 PEFLTRPSLITVDYPAPEVDITLTFEPRSNV--PDSEMDIIRLRPALSRGTAFS 297
DB 240 PNFISKPSFTITPDNPAEPMDITLTFESADSHVADDPDLILHRPALSRGTAFS 299
OY 298 RLGGRAIMFTSRGQIGARVHYHDISPIASPEXIEIQPIVSATE-DNGLEFDIYADDID 356
DB 300 RLGGKATLTKRSKQIGAKVHYHDISPIATEIEIQPLITSEHSTPLEDYVA-DAD 358
OY 357 PAMPVPSRPTSSAVSTSPITSSASYS--NVTPLTSSMDVPTTGPDTLP-PTSVW 413
DB 359 PAMPFTPTSTPTPTPRSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTW 418
OY 414 PIVSPTTASTOYIGIHGTHYILMPLYFYIPK-KRRKRVYFADGFA 460
DB 419 PYIPPPPTTMSHVAAGCNYYIMPYILIKRRKRRKRVCFSSGLAA 466

RESULT 7
O9DHD4 PRELIMINARY; PRT; 472 AA.
AC O9DHD4.
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Putative L2 protein.
GN L2.
OS Human papillomavirus type 87.
OC Viruses; dsDNA viruses, no RNA stage: Papillomaviridae;
OC Papillomavirus.
NCBI_TaxID=120381;
RN [1]

RP SEQUENCE FROM N.A.
RA Menzo S., Monachetti A., Trozzi C., Delius H., Clementi M.;
RT "Complete nucleotide sequence of candidaPV87.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ400628; CAC17717.2; -
DR InterPro; IPR000784; Late_L2.
DR Pfam; PF00513; late_protein_L2; 1
SQ SEQUENCE 472 AA; 50340 MW; E740C9C3C5CD481B CRC64;

Query Match 61.2%; Score 1472.5; DB 12; Length 472;
Best Local Similarity 63.4%; Pred. No. 9,6e-91;
Matches 301; Conservative 61; Mismatches 86; Indels 27; Gaps 12;

OY 7 ARRRASVTDLYKTKCKSGTCDVYNNKVEGTTLADKILQMSLGIPLGIGIGTSGTG 66
DB 4 SRRKRASVTDLYKTKCKVGTCPADVVPKEVDITLADIKMASLGVEFGIGIGTSGTG 63
OY 67 GRTGYPLGGRSNVVDYGPTRPVYIEPPTDPTSTLTLEDSSVYTSAPRPTGT 125
DB 64 GRTGYPLGRTPTPVVDYGPTRPVYIEPVGADPSTVTLVESSVINSGAPPPNFTGT 123
OY 126 SGFDITSAGTTTAVLDITPSTSVSISTNTNPAFSDPILIEVPGCEVSGNFGTP 185
DB 124 GGFVYTTSTTTPAVLDITPSSGVYVSTYINPLTFEPSTIIPVAGDAGHYLGTGTA 183
OY 186 TSGTHGEIYDLPOTFA--SGTGEPISTPLPTVRVAGPR--LYSKAYQOVANPEFL 242
DB 184 TSGTHGEIYDLPOTFAVAGGQGEPISTPIGVRRLAGRLNYSKAYQOVPTDASFL 243
OY 243 TRPSLITVDYPAPEVDITLTFEPRSNV--PDSEMDIIRLRPALSRGTAFSRLQ 301
DB 244 SRPSEVYTHNPMDEPSTLTFEPRSLHAPDPDLITLHRPALSRGTAFSRLQ 303
OY 302 RATMFTSRGQIGARVHYHDISPIASPEXIEIQPIVSAT--EDNGLEFDIYADDI---- 355
DB 304 RASRTRSGKRIIGARVHYHDISPIARA-DEIEIQPLVSTTAPSDDTLIDYADDTLSS 362
OY 356 ---DPAMFV--PSRPTSSAVSTSPITSSASYSNTVPLTSSMDVPTTGPDI----T 406
DB 363 VLKRPSPSLTSSSPPTASTKVSAT--ILSSSHDNTVPL-SATDVPYLTGPDIDHSA 419
OY 407 LPTSVMPYPTLPASTOYIGIHGTHYILMPLYFYIPKRRKRVYFADGFA 461
DB 420 PSPPTPVVPSSTAPYS---YIQQSDYLLPLNTIIFPKRRKRVYFSSDGFVA 471

RESULT 8
O9WNM5 PRELIMINARY; PRT; 471 AA.
AC O9WNM5.
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Minor capsid protein.
GN L2.
OS Human papillomavirus type 83.
OC Viruses; dsDNA viruses, no RNA stage: Papillomaviridae;
OC Papillomavirus.
NCBI_TaxID=96240;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99335608; PubMed=10405368;
RA Brown D.R., McClellan T.L., Woods K., Fife K.H.;
RT "Nucleotide sequence and characterization of human papillomavirus type 83, a novel genital papillomavirus.";
RL Virology 260:165-172(1999).
GN [2]
RP SEQUENCE FROM N.A.
RA Brown D.R., McClellan T.L., Woods K., Fife K.H.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF151983; AAD38973.1; -
DR InterPro; IPR000784; Late_L2.
DR Pfam; PF00513; late_protein_L2; 1.

Db 6 SRRKASATDLRTKASGTCPADYVPKVEGDTLADRIKMASLGEVFGGLIGTSSGSG 65
 QY 67 GRTGYIPLGGRSNVVDVGP-RRPVIEVPVPTDPSIYTLIEDSSVYSGAPRPTGCT 125
 Db 66 GRTGYIPLGTRPTVVDVGPTRAPPVIEVPVATDPSIYTLVEDSSVYAGAPLRFNCT 125
 QY 126 SGFDITSAGTTTPAVLDITPSSVSISTNTNPAFSDPSIIEVPQEGVSGNVFVCTP 185
 Db 126 GGFETVTSSTTTPAVLDITPSSVSISVSSSTYNPLFTEPSTIEVQADIDGHVLSSTA 185
 QY 186 TSGTGYEELPLOTFA-SGCTGEEPISSPPLTFRVAGPR--LYSRAVOQSVANPELT 242
 Db 186 TSGTGYEELPLOTFA-SGCTGEEPISSPPLTFRVAGPR--LYSRAVOQSVANPELT 245
 QY 243 TRPSSLITVDNPAFEVDVDTLTFEPRS--NVPSDFMDIIRLRPALTSRRGVRSRLG 300
 Db 246 SPPDSFVFPEDNVPYD-DETIIEFHPSLAPDPDFLDIYTLRPALTRARSGVRSRLG 304
 QY 301 QATMTFRSGTIGARVHFYHDISPAPSEYIELOPLVSATNEDNG-----LFDIYAD 353
 Db 305 QKASMKTRSGKHIGARVHFYHDLSPDAQ-EDIEILOPL-GAATSSGQSGQDTLYDIYAD 362
 QY 354 D--IDPAMPVPSRPTSSAVSTYSPYSS--ASSYSNVVPLSSMDVPYTGPD-- 404
 Db 363 DTHLSSTIQEPSPVSLHSTTPYSSATVSATSMVSTYDNTVPLSSATEVPLXTGPDIDH 422
 QY 405 -ITLPTSVMPVSPAPASTOY-IGIHGTHYMLPLYFIPKRRKRVFFPADGVAA 461
 Db 423 AIAPSPTPLPVPV---PSTPYAIYICGSDYLLPNYIFPFRKRRVHVSFSDGVAA 477

RESULT 11

Q99FW8 PRELIMINARY; PRT; 474 AA.
 AC 099FW8;
 DT 01-JUN-2001 (TREMREL. 17, Created)
 DT 01-JUN-2001 (TREMREL. 17, Last sequence update)
 DT 01-OCT-2001 (TREMREL. 18, Last annotation update)
 DE Putative minor capsid protein L2.
 GN L2.
 OS Human papillomavirus type 84.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus
 OX NCBI_Taxid=150546;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=2106735; PubMed=11145894;
 RA Terai M., Burk R.D.;
 RT *Complete Nucleotide Sequence and Analysis of a Novel Human
 RT Papillomavirus (HPV 84) Genome Cloned by an Overlapping PCR Method.*;
 RT Virology 279:109-115(2001).
 RN [2]
 RN SEQUENCE FROM N.A.
 RA Burk R.D., Terai M.;
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBD databases.
 DR EMBL: AF293960; AK09276.1; -
 DR InterPro: IPR000784; Late_L2.
 DR Pfam: PF00513; late_protein_L2.
 SQ SEQUENCE 474 AA; 50608 MW; 04BD0ECAED298551 CRC64;

Query Match 59.4%; Score 1429.5; DB 12; Length 474;

Best Local Similarity 62.6%; Pred. No. 7.3e-88; Matches 293; Conservative 55; Mismatches 105; Indels 15; Gaps 9;

QY 8 RRRKASVDDLKTCQSGTCPSDVVNKYEGTTLADKILQMSLGIIFLGIGTSGTSG 67
 Db 7 RRRKASVDDLKTCQSGTCPSDVVNKYEGTTLADKILQMSLGIIFLGIGTSGTSG 66
 QY 68 RTGYIPLGGRSNVVDVGP-RRPVIEVPVPTDPSIYTLIEDSSVYSGAPRPTGCT 126
 Db 67 RTGYIPLGTRPTVVDVGPTRAPPVIEVPVATDPSIYTLVEDSSVYAGAPLRFNCT 126
 QY 127 GFDITSAGTTTPAVLDITPSSVSISTNTNPAFSDPSIIEVPQEGVSGNVFVCTP 186

Db 127 GFEVTSSTTTPAVLDITPSSVSISVSSSTYNPLFTEPSTIEVQADIDGHVLSSTA 186
 QY 187 SGTGHEEELPLOTFA-SGCTGEEPISSPPLTFRVAGPR--LYSRAVOQSVANPELT 243
 Db 187 SGTGHEEELPLOTFA-SGCTGEEPISSPPLTFRVAGPR--LYSRAVOQSVANPELT 246
 QY 244 RPSLITVDNPAFEVDVDTLTFEPRS--NVPSDFMDIIRLRPALTSRRGVRSRLG 302
 Db 247 RPSLITVDNPAFEVDVDTLTFEPRS--NVPSDFMDIIRLRPALTSRRGVRSRLG 306
 QY 303 ATMTFRSGTIGARVHFYHDISPAPSEYIELOPLVSATNEDNG-----LFDIYAD 358
 Db 307 ASMRTRSGKHIGARVHFYHDLSP-PILEDIELOPLVSATNEDNG-----LFDIYAD 365
 QY 359 MPVS-----RPTSSAVSTYSPYSS--ASSYSNVVPLSSMDVPYTGPD-- 414
 Db 366 LRPVSALRKASPPASDLSATSTASTYDNTVPLSSGTDVPTTTPDIDHSAAPSAP 425
 QY 415 IVSPTAPASTOY-IGIHGTHYMLPLYFIPKRRKRVFFPADGVAA 461
 Db 426 PVPVTPSTPYAIYICGSDYLLPNYIFPFRKRRVHVSFSDGVAA 473

RESULT 12

Q82002 PRELIMINARY; PRT; 466 AA.
 AC Q82002;
 DT 01-NOV-1996 (TREMREL. 01, Created)
 DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
 DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
 DE Late gene.
 GN L2.
 OS Human papillomavirus type 72.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus
 OX NCBI_Taxid=51032;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=96213783; PubMed=8635859;
 RA Voelter C., He Y., Dellus H., Roy-Burman A., Greenspan J.S.,
 RA Greenspan D., de Villiers E.M.;
 RT *Novel HPV types present in oral papillomatous lesions from patients
 RT with HIV infection.*;
 RL Int. J. Cancer 66:453-456(1996).
 DR EMBL: X94164; CA63878.1; -
 DR InterPro: IPR000784; Late_L2.
 DR Pfam: PF00513; late_protein_L2.
 SQ SEQUENCE 466 AA; 49709 MW; B3D06F43227BDA0 CRC64;

Query Match 58.9%; Score 1417.5; DB 12; Length 466;

Best Local Similarity 61.1%; Pred. No. 4.6e-87; Matches 286; Conservative 66; Mismatches 93; Indels 23; Gaps 10;

QY 8 RRRKASVDDLKTCQSGTCPSDVVNKYEGTTLADKILQMSLGIIFLGIGTSGTSG 67
 Db 7 RRRKASVDDLKTCQSGTCPSDVVNKYEGTTLADKILQMSLGIIFLGIGTSGTSG 66
 QY 68 RTGYIPLGGRSNVVDVGP-RRPVIEVPVPTDPSIYTLIEDSSVYSGAPRPTGCT 126
 Db 67 RTGYIPLGTRPTVVDVGPTRAPPVIEVPVATDPSIYTLVEDSSVYAGAPLRFNCT 126
 QY 127 GFDITSAGTTTPAVLDITPSSVSISTNTNPAFSDPSIIEVPQEGVSGNVFVCTP 186
 Db 127 GFEVTSSTTTPAVLDITPSSVSISVSSSTYNPLFTEPSTIEVQADIDGHVLSSTA 186
 QY 187 SGTGHEEELPLOTFA-SGCTGEEPISSPPLTFRVAGPR--LYSRAVOQSVANPELT 243
 Db 187 SGTGHEEELPLOTFA-SGCTGEEPISSPPLTFRVAGPR--LYSRAVOQSVANPELT 246
 QY 244 RPSLITVDNPAFEVDVDTLTFEPRS--NVPSDFMDIIRLRPALTSRRGVRSRLG 301
 Db 247 RPSLITVDNPAFEVDVDTLTFEPRS--NVPSDFMDIIRLRPALTSRRGVRSRLG 305

QY	302	RATFETRSGTQIGAVHVFYHDI	SPAPSEVETELQPLV	SATDNGLFEDYADIDP	PAMPY 361				
Db	306	RATLRTBGRKRGIGAVHVFYHDI <th>SPISPL--SSDTIEM</th> <th>SSLASTIPDIT</th> <th>YDIA---DPDLGE 360</th>	SPISPL--SSDTIEM	SSLASTIPDIT	YDIA---DPDLGE 360				
QY	362	PSRPTTSSAVSTYSP <th>TISSASS----</th> <th>YSNWTVPLTSSMDV</th> <th>PYTGDTTL---PPTSW 413</th>	TISSASS----	YSNWTVPLTSSMDV	PYTGDTTL---PPTSW 413				
Db	361	PPPRASVSTSLHSP <th>SLSSASAKYD</th> <th>VNVP</th> <th>PLSGPHIPASSGPDIDLSPAPAVPTM 420</th>	SLSSASAKYD	VNVP	PLSGPHIPASSGPDIDLSPAPAVPTM 420				
QY	414	PIVSTPAASTOYIGIHG <th>HTYLMPLYFI</th> <th>PKRRKRP</th> <th>PFEEFDGYAA 461</th>	HTYLMPLYFI	PKRRKRP	PFEEFDGYAA 461				
Db	421	PLVPSTPHS--- <th>IYEGCFDEFLPAYIF</th> <th>FFPKRRKRPV</th> <th>SEFADGEVAA 465</th>	IYEGCFDEFLPAYIF	FFPKRRKRPV	SEFADGEVAA 465				
RESULT 13									
ID	08UTB8	PRELIMINARY: PRT: 456 AA.							
AC	08UTB8:								
DT	01-OCT-2002	(TREMBLrel. 22, Created)							
DT	01-OCT-2002	(TREMBLrel. 22, last sequence update)							
DT	01-MAR-2003	(TREMBLrel. 23, last annotation update)							
DE	Putative minor capsid protein L2.								
GN	L2.								
OS	Human papillomavirus type 89.								
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;								
OC	Papillomavirus.								
OX	NCBI_TaxID=202250;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=2207981; PubMed=12085327;								
RA	Teral M., Burk R.D.;								
RT	"Identification and Characterization of 3 Novel Genital Human								
RT	Papillomaviruses by Overlapping Polymerase Chain Reaction: candidHPV9,								
RT	candidHPV90, and candidHPV91.";								
RL	J. Infect. Dis. 185:1794-1797(2002).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RA	Burk R.D.;								
RL	Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.								
DR	EMBL: AF436128; AAM92156.1; -								
DR	InterPro: IPR000784: Late_L2.								
DR	Pfam: PF00513: late_protein_L2.1.								
SO	SEQUENCE 456 AA; 48182 MW; 8EA439BE300C9C47 CRC64;								
Query Match									
Best Local Similarity		55.3%; Score 1331; DB 12; Length 456;							
Matches 267; Conservative		70; Mismatches 88; Indels 16; Gaps 10							
QY	2	VSHRAARRKASV	VDLYTKTCQSGT	CPSPDVN	VNKRVEGTTLADKILQMSLIGIFLGIGIGT 61				
Db	1	MTHPRRRRKRAS	VTDLRYTKCATG	CPSPDVIR	PKVEGNLTADKILKMASLGVEFGIGIGT 60				
QY	62	GSGGGRGRGVI	PLDGRSM	TVVDVNGT -	RPVYIEVGVPRDSITVLLIESSSVYTSGARPP 120				
Db	61	SSGSGGRGRGVI	PLGRPTVVDVNGT	PARPVVIE	GVGAEPIVNLVEBSSIVESGAVLP 120				
QY	121	TFGTGSGDFIS	AGTTTAAVLDIT	PSSSTSIS	TNTFTNTPNAPSDSIEIVPOTGEVSGNV 180				
Db	121	NFTGDEGEIIT	SSSTTTPAVLIDIT	PSGATVQY	SSSYSPNAPATERSIIIEPPHGSVSGIV 180				
QY	181	FVGIVTSGTHGE	EIPLDTFAS	SGTGEER-PI	STPLPIYRVYAGPR -LYSRAYQOVSA 237				
Db	181	FTSTPTSSHTE	EEELIPMSFT	AGSGVNDAGPI	STPVPGVRIAGPRLNYSKATQOVPS 240				
QY	238	NPEFLTRSS	LITVYNNPA	FEPPDTLLIF	PPRSNV-PPDSFMDILRLHRAPLSRKGTVPF 296				
Db	241	DSAFVSRPAS	FEYTVNPNV	DEPETLLIF	FEHPDLHAPDPPEFLVVALHRAPLSRKGTVPF 300				
QY	297	SLTSGARAME	TFSTQIGARV	FHYFDIS	PIASPEYIEIQLQPLVSATE -DNGLFDIYAD-- 353				
Db	301	SNVGGRA	TLKTRKISG	QIGARV	FHYFDIVSPIS -AAESIEMQPLPSPDQLQPYVDIADTT 359				
QY	354	DIDPAMPVP	SRPTTSSAV	STVS-PTISS--	ASSTSNVTVPLTSSMDVVPYTGDTTLF 408				

Dd		360	HLDVLAERPPAPASSANTFTSGPIYATFSAVSSQYTWVTPLSGGFVPVAVTGPDIANP	419
Oy		409	PTSWMPLYSP--TAPASQTYI 427	
Dd		420	TAPSVPPIFPSTYLGPSTGYI 440	
 RESULT 14 O8JTG3				
ID	O8JTG3	PRELIMINARY;	PRT; 460 AA.	
AC	O8JTG3;			
DT	01-OCT-2002 (TREMBLrel. 22, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Putative minor capsid protein L2.			
GN	L2.			
OS	Human papillomavirus type 91.			
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;			
CC	Papillomavirus.			
OX	NCBL_TaxID=202252;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22079861; Pubmed=12085327;			
RA	Teral M., Burk R.D.;			
RT	"Identification and Characterization of 3 Novel Genital Human			
RT	Papillomaviruses by Overlapping Polymerase Chain Reaction: candHPv9,			
RT	candHPv90, and candHPv91."			
RL	J. Infect. Dis. 185:1794-1797(2002).			
RP	[2]			
RN	SEQUENCE FROM N.A.			
RA	Burk R.D., Teral M.;			
RL	Submitted (SEP-2001) to the EMBL/Genbank/DDBJ databases.			
DR	EMBL; AF419318; AAM89135.1; -			
DR	InterPro: IPR000784; Late_L2.			
DR	Pfam: PF00513; late_protein_L2; 1			
SQ	SEQUENCE 460 AA; 49194 MW; 0D6D63DBD3C8B69 CRC64;			
 Query Match 48.5%; Score 1166.5; DB 12; Length 460; Best Local Similarity 51.5%; Pred. No. 3e-70; Matches 246; Conservative 75; Mismatches 122; Indels 35; Gaps 15;				
Oy		1	MVSHRAARRKASYVDLTAKTKOSTGCSQSDVNVEGTTLADKLQWSLGIFGLGIG 60	
Dd		1	MVSTILKRKKRKAATQLQTCKAGTCPSDVINKKEHTTADQLIKWMSKGVFEGLGIG 60	
Oy		61	TGSGTGRTGYIPL-GGRSNTVVNDGP-----TRPPVIEEVPGPSIVTLIEDSSVYT 114	
Dd		61	TGSGSGGGRTGVPLPTGRTGVPKKSANBPVVSRRPVVIEEPVAPIDPSIVLSIESSLTE 120	
Oy		115	SGARPPTTGTSGSDPDITSAGTTTPAVALDITPSSISVISISTNFNTNPADSPTSIEVPOTG 174	
Dd		121	SGAPTTTTPHSGGGEVTSGSDDVAIPALDYSV-TTSVHVTYTTTHLPATDPDAIVQPTPEPL 179	
Oy		175	EVSNGVNEFGTPTSGHGHEEYPLQFGFASSGGESEISTPLPYTVRVARGPR--LYSRAYO 232	
Dd		180	EAGRIIIISOGTIHAHSADIIPMOTFV---VHSDPLTSTPPL--GNASRPRLGLYSKALQ 234	
Oy		233	QVSVANPEELTRPSSLITYDNPAEEPVDTTLFEERS--NVPSDSFDMDIRLRPALTRS 290	
Dd		235	QIEIYDFAFLLSSPOLRTIYDNPVDEFDDPATIAFEQPVHEAPADSFMFOIVTLHRPALNSR 294	
Oy		291	RGTVAFESLGRATMTFRSSGOIGARKVFFHDISIASPETIEQLP----VSATIEDNG 346	
Dd		295	RGLVAFESVGAGVIYTRSGIRIGERVHFEDIISA-TQESIETQPLGHSTVNPADTD 353	
Oy		347	LFEDIYADDIDAMPAPRSRPTTSSAAVSTPTISSASSSNVTVPLTSSGDVPPVYTGPDIT 406	
Dd		354	LYDIYAAD-----SLDYVPKINTVNS----FLPNKTIVNTTVPLATVPDITLQAGPDIT 404	
Oy		407	LP--PTSWMPLYSPAFAST-QYISGHTHYIYMLPLYFIKKRKRVYFFRADGVAA 461	
Dd		405	FPTVPLAVS-PVY-PLSPSPVTPSAVSIYGTDFVLHSLHFGFKRRRIYFFPADNVAA 460	

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RESULT 15
ID 081016 PRELIMINARY; PRT; 466 AA.
AC 081016;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE L2 capsid protein.
OS Human papillomavirus type 31.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10585;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS2;
RX MEDLINE=96130211; PubMed=8553573;
RA Icenogle J.P., Clancy K.A., Lin S.Y.;
RT "Sequence variation in the capsid protein genes of human
RL papillomavirus type 16 and type 31.";
RT Virology 214:664-669(1995).
DR EMBL: U37410; AAA92893.1; -.
DR InterPro: IPR000784; Late_L2;
DR Pfam: PF00513; late-protein_L2; 1.
SQ SEQUENCE 466 AA; 50040 MW; 125438BD13A83412 CRC64;

Query Match 48.3%; Score 1160.5; DB 12; Length 466;
Best Local Similarity 50.9%; Pred. No. 7,66-70;
Matches 247; Conservative 78; Mismatches 117; Indels 43; Gaps 15;

QY 1 MYSRAAR-KRASVDLYKCTCKSGTCDVNVKVEGTLADKILQMSLGIPLGLGI 59
   | | : : | | | | : | | | | : | | | | : | | | | : | | | |
Db 1 MRSKRSTKTKRASATOLYCTKAGCPSDVIPIKIEHTIADQILRYSMGVFEGLGI 60
-QY 60 GTSGGTGGRGYIPLGSRNTYVDG--PTRBPVYIEPYGTPDPSTVTLIEDSSVYTSAP 118
   | : | | | | | | | | : | | : | | | | | | | | | | | | : | |
Db 61 GSGGTGGRGYIPLGSRNTYVDG--PTRBPVYIEPYGTPDPSTVTLIEDSSVYTSAP 120
QY 119 R-PTFGTSGEDITSAGTTTTPAVLIDITPSSTSVSIITNFTNPATFSDPSIIEVPTGEV 176
   | | | | | | | | : | | | | : | | | | : | | | | : | | | |
Db 121 APIRPPPTSGEDITATADTPTALDVT-----SVST--HENPTFDPSVLQPTPAET 172
QY 177 SGANFVGTPTSGTGYEIPQLQTFASSGTGEPISSTPLPTVRRVAGPRLYSRAYQOVS 236
   | : : : : | | | | | | | | | | | | | | | | | | | | | |
Db 173 SGHLSSSSISSTHNYEIPMDTFIVSTNNENITSTPIPGVRRPARGLYSKATQOVKY 232
QY 237 ANPEFLRPSLITYDNPAPFV--DTTLFEPKSN--VPDSDMDIIRLHRPALTSRSG 292
   | | | : | | | | | | | | : : | | : | | | | | | | | | |
Db 233 IDPFLSLPKOLITYENPAITVNAESLFSNTSHMKAPDPDFLDITLHRPALTSRKN 292
QY 293 TVRSRLGORATMFTRSQTQIGARVHFYHDISPIAPSPXYTELQPL-----VSATEDNGL 347
   | | | | | : | | | | | | | | | | | | | | | | | | | | |
Db 293 TVRSRLGNKQTLTRSGATIGARVHYIIDSSINPAGESIEMQPLGASATTTSTINDGL 352
QY 348 EDIYADIDPAMPVPS-----RPTT-----SSAVSTYSPTISSASSISNTVPLTSSMDVPV 399
   | | | | | : | | : | | | | | | | | | | | | | | | | |
Db 353 YDIYA-DTDFVVDPPATHNWSPSTALQSTSAVAYVP-----NTTVPLSTGFDPI 403
QY 400 YTGPDITL--PPTSVWVIVSPATAPASQY-IGIGHTHYLLPLVYFIIPKRRKRVYEPFAD 456
   | | | | : | | | | | | | | | | | | | | | | | | | | |
Db 404 FSGPDVPIENAPTOVFP--PLAFTTPOVSLFVDGDFYLLHPSYMLKRRKRKVSFEFTD 461
QY 457 GFVAA 461
   |||
Db 462 VSVAA 466
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Search completed: October 17, 2003, 11:02:08
Job time : 66.9112 secs

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OM protein - protein search, using sw model

Run on: October 17, 2003, 11:02:14 : Search time 47.6622 Seconds

(without alignments)
1743.646 Million cell updates/sec

Title: US-08-913-644-2

Perfect score: 2733
Sequence: 1 MALMRSDNTVYLPSPSVAR.....APSATSSKPAKRVRRARK 507

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 609560 seqs, 163917102 residues

Total number of hits satisfying chosen parameters: 609560

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
Published Applications_AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2705	99.0	568	11	US-09-991-053-3
2	2705	99.0	568	15	US-10-301-260A-3
3	1831	67.0	505	10	US-09-162-904A-4
4	1826	66.8	505	10	US-09-824-017-2
5	1826	66.8	505	11	US-09-986-118A-2
6	1825	66.8	505	10	US-09-162-904A-3
7	1820.5	66.6	502	12	US-10-224-999A-3469
8	1801	65.9	531	11	US-09-991-053-1
9	1801	65.9	531	15	US-10-301-260A-1
10	1324.5	48.5	508	9	US-09-134-377-1
11	1298	47.5	508	10	US-09-822-662-1
12	1298	47.5	503	9	US-09-134-377-2
13	1298	47.5	503	10	US-09-822-662-2
14	1283	46.9	495	12	US-10-305-765-2
15	1283	46.9	495	12	US-10-305-765-4

16	1283	46.9	495	12	US-10-305-633-2	Sequence 2, Appl1
17	1283	46.9	495	12	US-10-305-633-4	Sequence 4, Appl1
18	604	22.1	132	14	US-10-056-359-29	Sequence 29, Appl1
19	604	22.1	132	14	US-10-056-360-29	Sequence 29, Appl1
20	551.5	20.2	151	12	US-10-224-999A-3467	Sequence 3467, Ap
21	374	13.7	144	14	US-10-056-359-5	Sequence 5, Appl1
22	374	13.7	144	14	US-10-056-360-5	Sequence 5, Appl1
23	363	13.3	136	14	US-10-056-359-8	Sequence 8, Appl1
24	363	13.3	136	14	US-10-056-360-8	Sequence 8, Appl1
25	359.5	13.2	139	14	US-10-056-359-2	Sequence 2, Appl1
26	359.5	13.2	139	14	US-10-056-360-2	Sequence 2, Appl1
27	353.5	12.9	145	14	US-10-056-359-11	Sequence 11, Appl1
28	353.5	12.9	145	14	US-10-056-360-11	Sequence 11, Appl1
29	353	12.9	138	14	US-10-056-359-23	Sequence 23, Appl1
30	353	12.9	138	14	US-10-056-360-23	Sequence 23, Appl1
31	352	12.9	138	14	US-10-056-359-14	Sequence 14, Appl1
32	352	12.9	138	14	US-10-056-360-14	Sequence 14, Appl1
33	351	12.8	142	14	US-10-056-359-20	Sequence 20, Appl1
34	351	12.8	142	14	US-10-056-360-20	Sequence 20, Appl1
35	333.5	12.2	137	14	US-10-056-359-17	Sequence 17, Appl1
36	333.5	12.2	137	14	US-10-056-360-17	Sequence 17, Appl1
37	331.5	12.1	141	14	US-10-056-359-26	Sequence 26, Appl1
38	331.5	12.1	141	14	US-10-056-360-26	Sequence 26, Appl1
39	109	4.0	967	12	US-10-032-189-38	Sequence 38, Appl1
40	101.5	3.7	5701	9	US-09-864-761-37319	Sequence 37319, A
41	100.5	3.7	26926	10	US-09-759-508B-2	Sequence 2, Appl1
42	94.5	3.5	710	15	US-10-296-770-4	Sequence 4, Appl1
43	94.5	3.5	777	14	US-09-765-111A-2	Sequence 2, Appl1
44	90.5	3.3	788	10	US-10-003-152-6	Sequence 6, Appl1
45	90.5	3.3	788	15	US-10-002-050-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-09-991-053-3
; Sequence 3, Application US/0991053
; Publication No. US20030003532A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen
; TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
; FILE REFERENCE: Harvard/Harrison 12687/1120
; CURRENT APPLICATION NUMBER: US/09/991,053
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-18
; PRIOR APPLICATION NUMBER: 60/125208
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/148544
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-09-991-053-3

Query Match 99.0%; Score 2705; DB 11; Length 568;
Best Local Similarity 99.0%; Pred. No. 7.6e-271;
Matches 502; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
DB 122 DIRKVSAYQYRVVQLPDKRFGLLPDTSTINPETORLWACAGVEIGKQPLGVGLSH 181

Qy	121	PFYFNKJDDHSSHAATSNSYSEVVRNNSVDYQOTDCLIGCAPAIGHEMAGTACKSRPL	180
Db	182	PFYFNKJDDHSSHAATSNSYSEVVRNNSVDYKQOTDCLIGCAPAIGHEMAGTACKSRPL	241
Qy	181	SQGDCCPPELEKNTVLEDDGMDVDTGYGAMDFTLQDCKEVPBLDIOCSICKKPYDLQMSAD	240
Db	242	SQGDCCPPELEKNTVLEDDGMDVDTGYGAMDFTLQDCKEVPBLDIOCSICKKPYDLQMSAD	301
Qy	241	PYGDSMFECFLRRQFLFARHFNNRAGTMGDYVQSLYIKGTGKRASPGSCVYSPSPSGSIY	300
Db	302	PYGDSMFECFLRRQFLFARHFNNRAGTMGDYVQSLYIKGTGKRASPGSCVYSPSPSGSIY	361
Qy	301	TTSOQLFENRPFYMLHKRQGNNGICQHNOLEFYVVDTRSTNLTICASTQSPQOYATK	360
Db	362	TTSOQLFENRPFYMLHKRQGNNGICQHNOLEFYVVDTRSTNLTICASTQSPQOYATK	421
Qy	361	FKQSRHVEEYDLOFIQOLCTITLLADVMSYISHSNSSILDEDMNFGVPPPTTSLVDYTR	420
Db	422	FKQSRHVEEYDLOFIQOLCTITLLADVMSYISHSNSSILDEDMNFGVPPPTTSLVDYTR	481
Qy	421	FVQSVAITCQKDAAPENKDPYDKLKFNNVDLKEFSLDDQYPLGRKFLVQAGLRKPT	480
Db	482	FVQSVAITCQKDAAPENKDPYDKLKFNNVDLKEFSLDDQYPLGRKFLVQAGLRKPT	541
Qy	481	IGPRKRSAPATSSSPAKRRVVRARK	507
Db	542	IGPRKRSAPATSSSPAKRRVVRARK	568

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RESULT 2
US-10-301-260A-3
Sequence 3, Application US/10301260A
Publication No. US20030118609A1
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen
APPLICANT: Chen, Xiaojiang
TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
FILE REFERENCE: Harvard/Harrison 12687/1123
CURRENT APPLICATION NUMBER: US/10/301,260A
CURRENT FILING DATE: 2002-11-21
PRIORITY APPLICATION NUMBER: 09/520,822
PRIORITY FILING DATE: 2000-03-18
PRIORITY APPLICATION NUMBER: 60/125208
PRIORITY FILING DATE: 1999-03-18
PRIORITY APPLICATION NUMBER: 60/148544
PRIORITY FILING DATE: 1999-08-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 568
TYPE: PRF
ORGANISM: Human papillomavirus type 18
US-10-301-260A-3

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	Query Match	99.0%	Score 2705:	DB 15:	Length 568:
	Best Local Similarity	99.0%	Pred. No. 7,66-271:		
	Matches	502:	Conservative	1:	Mismatches 4: Indels 0: Gaps 0:
QY	1	MALMRPSDNITYLLEPPSYARVYNTDDYTRKSIIFYHAGSSRLTYGNPFYRVYPAGGANKQ	60		
Db	62	MALMRPSDNITYLLEPPSYARVYNTDDYTPSIFYHAGSSRLTYGNPFYRVYPAGGANKQ	121		
QY	61	DIPKYSAYQYKVEFVQLDPPNKFGLPDMSINPFTQRLVMACAGYEIRGQPLGTLGSLGH	120		
Db	122	DIPKYSAYQYKVEFVQLDPPNKFGLPDPSIYNPFTQRLVMACAGYEIRGQPLGTLGSLGH	181		
QY	121	PFYKKLDDTSSHAATSNVSESDVDNYSVDYKKQOYLCLGCAPAIGEHMAGTACKSPL	180		
Db	182	PFYKKLDDTSSHAATSNVSESDVDNYSVDYKKOYLCLGCAPAIGEHMAGTACKSPL	241		
QY	181	SGQCDPLELKNVLEDDGWDVDTGAGADFSTLDQFKCEVPDLDTQSICTKPYDTQMSAD	240		

Db	24	SQGDCEPPELEKNTVLEDSGMVDTGYGAMDFSTLDQTKCEVPLDIOQSTICKXPDIQMSAD	301
QY	241	PYGDSMEFCLLRQQLFAHFENRAGTMDYVQSLIKGTGMKSPSGCYSPSPSGSIV	300
Db	302	PYDSDMEFCLLRQQLFAHFENRAGTMDYVQSLIKGTGMKSPSGCYSPSPSGSIV	361
QY	301	TSDSOLEFNKPYWLHKRQAGNNGICWHNOLFVIVVDTKSTMLTICASTOSPVPQOYATK	360
Db	362	TSDSOLEFNKPYWLHKRQAGNNGICWHNOLFVIVVDTKSTMLTICASTOSPVPQOYATK	421
QY	361	FKQSYHVEYDOLFEOICTTITLADWASYHSMNSSLIEDMNGVPEPTSLVDTYR	420
Db	422	FKQSYHVEYDOLFEOICTTITLADWASYHSMNSSLIEDMNGVPEPTSLVDTYR	481
QY	421	FVQSVAILTCQKDAPEANKDPYDKLFWNVDLKEKFSLLDOYPLGRKFLVOAGLRRKPT	480
Db	482	FVQSVAILTCQKDAPEANKDPYDKLFWNVDLKEKFSLLDOYPLGRKFLVOAGLRRKPT	541
QY	481	IGPRKRSAPATSSSKPAKRVYRPAK	507
Db	542	IGPRKRSAPATSSSKPAKRVYRPAK	568

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RESULT 3
US-09-162-904A-4
Sequence 4, Application US/09162904A
Patent No. US2002016872A1
GENERAL INFORMATION:
APPLICANT: Durst, Mathias
APPLICANT: Gissmann, Lutz
TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLOMAVIRUS L1 PROTEIN CAPABLE
TITLE OF INVENTION: OF EFFICIENTLY FORMING VIRUS-LIKE PARTICLES
FILE REFERENCE: 8484-068-999
CURRENT APPLICATION NUMBER: US/09/162,904A
CURRENT FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 08/884,168
PRIOR FILING DATE: 1997-06-27
PRIOR APPLICATION NUMBER: 08/641,570
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/902,528
PRIOR FILING DATE: 1993-07-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 505
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of L1
US-09-162-904A-4

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Query Match	Similarity	67.0%	Score 1831	DB 10	Length 505
Best Local	Similarity	66.5%	Pred. No. 26-180		
Matches	Conservative	68	Mismatches	96	Indels 4; Gaps 3;
QY	1	MALRRPSDNVYLLPPPSVARYVNDIDYTRISIEYHAGSSRLITVGNPFYRVDPAGGNKQ	60		
Db	1	MSLMLPSATVYLLPPVPVSKVSTDEYAKRTIYHAGTSRLLAGVHPPIKPPNNKI	60		
QY	61	DIPKSAQYQYVRFROLDPNKFGLPDSIYNEPQRLVWACAGVEIGGQPLVLSGH	120		
Db	61	LVPKVSGLQYVRFRLHLPDPNKFGLPDSIYNEPQRLVWACVGVGVGGQPLVLSGH	120		
QY	121	PFYKKLDDTESSHAATSVSESDVARDNVSDVKQIOLCLIGCAPAIGEHMAKTSACKRPL	180		
Db	121	PLTKKLDDTEENASAAVANAAGVDNRECIISMDYKOTOLCLIGCKRPIGEHMGKSPCTNNAV	180		
QY	181	SGQGGPPELKNVTVLEDGDMDVDTGCGAMDEFSTLOTKCEVPLDIOSTICKYDYLQMSAD	240		
Db	181	NPGGCPPELKNVTVIQDGDMDVDTGCGAMDEFSTLOTKANKSEVPPLDICTSICKYDYLIKWSE	240		
QY	241	PYGDSMFQCLRRDLEFAHFENNRACMGTDYVQSLYIKGTGNRASPGSCVSPSPGSLV	300		

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Db      241 PEGDGLFPLRREQFVRLHFNRACTGENVDDLIYKSGSTANLASSNTPTPSGSNV 300
Qy      301 TSDSOLFKNRPMYLHKAQGNNGICMHNOLFVTVVDTRSTNTLICASSTPSYGOYDARK 360
Db      301 TSDAQIFKNRPMYLQRAQGNNGICMGNOLFVTVVDTRSTNTSLCAAI-STSETTYKKN 359
Qy      361 FKQYSRHVEYDLOQIFOLCKITTLTADVMSYIHSNNSILEDNMFGVPPPTSLVDYR 420
Db      360 FKQYSRHVEYDLOQIFOLCKITTLTADVMTYIHSNNSITLEDNMFGLOPPPGTLEDYR 419
Qy      421 FVQSAITCQKDAAPENKDPYDKLFENVDLKEKFSLDLDQYPLGRKFLVQAGLRKP- 479
Db      420 FVTSQAIAQKHTPPAPKEDPLKTYFMEVNLKEKFSADLDQFPLGRKFLVQAGLRKP 479
Qy      480 -TIGPRKRSAPSATTSKPAKR 500
Db      480 FTLGRRK-ATPTSTSTTAKR 500

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RESULT 4

US-09-824-017-2

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; Sequence 2, Application US/09824017
; Publication No. US20020197668A1

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GENERAL INFORMATION:

APPLICANT: BORGES, Alexander

HALLER, Michael

TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE

FORMULATIONS AND METHODS OF USE

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/824, 017

FILING DATE: 03-Apr-2001

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026, 896

FILING DATE: 1998-02-20

ATTORNEY/AGENT INFORMATION:

NAME: Sandercock, Colin G.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37067/102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 2:

FILING DATE: 07-No. US20030021806A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/026, 896

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Sandercock, Colin G.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37067/102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 2:

FILING DATE: 07-No. US20030021806A1-2001

CLASSIFICATION: <Unknown>

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Qy      61 DIPKVASQYRVFRVLPDPNKFGLPDNSTYPEFOTRLVACAGVEITGQGLVGLSGH 120
Db      61 LVPKVSGLQYRVFRRLHLPDPNKFGLPDNSTYPEFOTRLVACAGVEITGQGLVGLSGH 120
Qy      121 PRYKTKDDTESSHAATSNVSEYDQVSVYDQKOTOCITGCAPAIGEHAKGTACKSRPL 180
Db      121 PLINKKDDTESSHAATSNVSEYDQVSVYDQKOTOCITGCAPAIGEHAKGTACKSRPL 180
Qy      181 SOGDCPPLKNTVLEDGDMVDYGYGAMDESTLQDKCEVPLDICSICKYDYLOMSAD 240
Db      181 NPGDCPPLKNTVLEDGDMVDYGYGAMDESTLQDKCEVPLDICSICKYDYLOMSAD 240
Qy      241 PYGDSMFELRLRQQLFARFNNRAGMGTVPQSLYIKGTGMRASGSCVPSBGSATY 300
Db      241 PYGDSMFELRLRQQLFARFNNRAGMGTVPQSLYIKGTGMRASGSCVPSBGSATY 300
Qy      301 TSDSOLFKNRPMYLHKAQGNNGICMHNOLFVTVVDTRSTNTLICASSTPSYGOYDARK 360
Db      301 TSDAQIFKNRPMYLQRAQGNNGICMGNOLFVTVVDTRSTNTSLCAAI-STSETTYKKN 359
Qy      361 FKQYSRHVEYDLOQIFOLCKITTLTADVMSYIHSNNSILEDNMFGVPPPTSLVDYR 420
Db      360 FKQYSRHVEYDLOQIFOLCKITTLTADVMTYIHSNNSITLEDNMFGLOPPPGTLEDYR 419
Qy      421 FVQSAITCQKDAAPENKDPYDKLFENVDLKEKFSLDLDQYPLGRKFLVQAGLRKP- 479
Db      420 FVTSQAIAQKHTPPAPKEDPLKTYFMEVNLKEKFSADLDQFPLGRKFLVQAGLRKP 479
Qy      480 -TIGPRKRSAPSATTSKPAKR 500
Db      480 FTLGRRK-ATPTSTSTTAKR 500

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RESULT 5

US-09-986-118A-2

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; Sequence 2, Application US/09986118A
; Publication No. US20030021806A1

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GENERAL INFORMATION:

APPLICANT: BORGES, Alexander

HALLER, Michael

TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE

FORMULATIONS AND METHODS OF USE

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/986, 118A

FILING DATE: 07-No. US20030021806A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/026, 896

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Sandercock, Colin G.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37067/102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 2:

FILING DATE: 07-No. US20030021806A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/026, 896

FILING DATE: <Unknown>

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-986-118A-2

Query Match      66.8%; Score 1826; DB 11; Length 505;
Best Local Similarity 66.3%; Pred. No. 6.7e-180;
Matches 333; Conservative 68; Mismatches 97; Indels 4; Gaps 3;

OY 1 MALMRPSDNTVYLPPEPSVARVNTDDVYTRTSIFHYHAGSSRLTLVGNPYRVPAGGKNQ 60
D 1 MSMLPSEATVYLPPEVSVSKVSTDEYVARTNTIYHAGTSRLAVGHHPYIRKPNKKI 60
OY 61 DIPVSAVQYRVFVQVLPDPNKGFLPDNSTIYNPETQRLVWACAGVEIGRQPLGVGSGH 120
D 61 LVPRVSGIQYRVFRIHLPDPNKGFPDTSFYNPDTQRLVWACAGVEIGRQPLGVGSGH 120
OY 121 PFYKRLDDESSHAATNSVEDVDNYSVDYKQOTOLICAPAIQGEHMAKGTACKSRPL 180
D 121 PLNKKLDDEENASVYANAGVDNRECSIMDKQFOLICGKPPIGEHMGKSPCTNVAV 180
OY 181 SGGDCPPELEKNTVLEDDGMDVDTGCGAMDFTLQDFCEVPLDLCOSICKPPYLQMSAD 240
D 181 NPGDCPPELEINTVIOGDMDVDTGCGAMDFTLQANSSEVPLDICTSICKPPYLQMSAD 240
OY 241 PYGSMFECRLREQLFARHFNRACTMGDIYPOSLYTKGTGMASPGSCVSPSGSIV 300
D 241 PYGSLFFYLRRQEMFARHFNRAAGAVENPDDLTKGSGSTANLASSNFFPPSGSMV 300
OY 301 TSDSQLEFNKPYWLKRAQGHNNICMHNQLEFVTVVDTTRSTNLTCASQSPVPGQYDATK 360
D 301 TSDAQINFKPYWLQRAQGHNNICMGNQLEFVTVVDTTRSTNMSLCAAI-STSETTYKNTN 359
OY 361 FKQYSRVVEEDLOFIFOLCTITLTADVMSYIHSNSSLIEDMNFQVPPPTSLVDYR 420
D 361 FKELLRGEEYDLOFIFOLCTITLTADVMTYIHSNSSLIEDMNFGLQPPGGTLEDTYR 419
OY 421 FVQSVATTCQKDAAPAEKNDPYDKLFKNVNDLKEKFSLDQYPLGRKFLVQAGLRKRP- 479
D 421 FVTSQALACQKHPPAPKEDPKKTYTFEWNLKEKFSADLDQPLGRKFLVQAGLRKRP 479
OY 480 -TIGPKRSAPSATTSKPAKR 500
D 480 FTIGKRRK-ATPTTSTSTTAKR 500

RESULT 6
US-09-162-904A-3
; Sequence 3, Application US/09162904A
; Patent No. US20020168372A1
; GENERAL INFORMATION:
; APPLICANT: Durst, Matthias
; APPLICANT: Gissmann, Jutz
; TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLOMAVIRUS L1 PROTEIN CAPABLE
; FILE REFERENCE: 8484-068-999
; CURRENT APPLICATION NUMBER: US/09/162, 904A
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/884,168
; PRIOR FILING DATE: 1997-06-27
; PRIOR APPLICATION NUMBER: 08/641,570
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/902,528
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 505.
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of L1 gen
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US-09-162-904A-3

Query Match      66.8%; Score 1825; DB 10; Length 505;
Best Local Similarity 66.1%; Pred. No. 8.5e-180;
Matches 332; Conservative 69; Mismatches 97; Indels 4; Gaps 3;

OY 1 MALMRPSDNTVYLPPEPSVARVNTDDVYTRTSIFHYHAGSSRLTLVGNPYRVPAGGKNQ 60
D 1 MSMLPSEATVYLPPEVSVSKVSTDEYVARTNTIYHAGTSRLAVGHHPYIRKPNKKI 60
OY 61 DIPVSAVQYRVFVQVLPDPNKGFLPDNSTIYNPETQRLVWACAGVEIGRQPLGVGSGH 120
D 61 LVPRVSGIQYRVFRIHLPDPNKGFPDTSFYNPDTQRLVWACAGVEIGRQPLGVGSGH 120
OY 121 PFYKRLDDESSHAATNSVEDVDNYSVDYKQOTOLICAPAIQGEHMAKGTACKSRPL 180
D 121 PLNKKLDDEENASVYANAGVDNRECSIMDKQFOLICGKPPIGEHMGKSPCTNVAV 180
OY 181 SGGDCPPELEKNTVLEDDGMDVDTGCGAMDFTLQDFCEVPLDLCOSICKPPYLQMSAD 240
D 181 NPGDCPPELEINTVIOGDMDVDTGCGAMDFTLQANSSEVPLDICTSICKPPYLQMSAD 240
OY 241 PYGSMFECRLREQLFARHFNRACTMGDIYPOSLYTKGTGMASPGSCVSPSGSIV 300
D 241 PYGSLFFYLRRQEMFARHFNRAAGAVENPDDLTKGSGSTANLASSNFFPPSGSMV 300
OY 301 TSDSQLEFNKPYWLKRAQGHNNICMHNQLEFVTVVDTTRSTNLTCASQSPVPGQYDATK 360
D 301 TSDAQINFKPYWLQRAQGHNNICMGNQLEFVTVVDTTRSTNMSLCAAI-STSETTYKNTN 359
OY 361 FKQYSRVVEEDLOFIFOLCTITLTADVMSYIHSNSSLIEDMNFQVPPPTSLVDYR 420
D 361 FKELLRGEEYDLOFIFOLCTITLTADVMTYIHSNSSLIEDMNFGLQPPGGTLEDTYR 419
OY 421 FVQSVATTCQKDAAPAEKNDPYDKLFKNVNDLKEKFSLDQYPLGRKFLVQAGLRKRP- 479
D 421 FVTSQALACQKHPPAPKEDPKKTYTFEWNLKEKFSADLDQPLGRKFLVQAGLRKRP 479
OY 480 -TIGPKRSAPSATTSKPAKR 500
D 480 FTIGKRRK-ATPTTSTSTTAKR 500

RESULT 7
US-10-224-999A-3469
; Sequence 3469, Application US/10224999A
; Publication No. US2003017318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavit, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004, 01
; CURRENT APPLICATION NUMBER: US/10/224, 999A
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313, 695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3469
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Human papillomavirus type 35
US-10-224-999A-3469

Query Match      66.6%; Score 1820.5; DB 12; Length 502;
Best Local Similarity 65.1%; Pred. No. 2.3e-179;
Matches 329; Conservative 70; Mismatches 103; Indels 3; Gaps 2;

OY 1 MALMRPSDNTVYLPPEPSVARVNTDDVYTRTSIFHYHAGSSRLTLVGNPYRVPAGGKNQ 60
D 1 MSMLRSEATVYLPPEVSVSKVSTDEYVARTNTIYHAGTSRLAVGHHPYIAIKKODSNKI 60
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```

QY 61 DLPKVSAYOYRFRVLOLDPNKGFLPDNSIYNFETORLWACAGVEIGRGQPLGVLGSH 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AYPKVSGLQYRFRVRLPDPNKGFPDTSFYDPAQRLWACAGVEIGRGQPLGVLGSH 120
QY 121 PFYNTKDDTRESSHAATSNVSEYRDVNVSDYKOTQCLIGCAPAIGEHNAKGTACKSRPL 180
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 PLINKLDDTENASAVYAMGVNDRRECIISMDYKOTQCLIGCKPPIEBHMGKSPCTNVAV 206
QY 181 SOGDCPPELEKNTVLEDGDMVDVGYGAMDESTLQDCKCEVPLDICKOSICKYPPYLQMSAD 240
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 KAGECPPELEKNTVLEDGDMVDVGYGAMDESTLQDCKCEVPLDICKOSICKYPPYLQMSAD 240
QY 241 PIGDSMFECILRRQLEFARHFNWAGMGDTVPQSLYIKGTGMARSPGSCVSPSPGSIY 300
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 PYGDSMFECILRRQLEFARHFNWAGMGDTVPQSLYIKGTGMARSPGSCVSPSPGSIY 300
QY 301 TSDSOLEFNKPYMLQKQGHNGICWGNOLFTVYVDDTRSTNLTICASTOSPVGQYDARK 360
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 TSDSOLEFNKPYMLQKQGHNGICWGNOLFTVYVDDTRSTNLTICASTOSPVGQYDARK 360
QY 361 FKQYSHREBYDQLEFQOLCTITLTDVMSYIHSNNSILEDNMFVGPPEPTSLVDYR 420
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 FKQYSHREBYDQLEFQOLCTITLTDVMSYIHSNNSILEDNMFVGPPEPTSLVDYR 420
QY 421 FVQSVATITQKDAAPAEKNDPYDKLFNWNVDLKEKESLDLDQYPLGRKFLVQAGLRKRP 480
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 FVQSVATITQKDAAPAEKNDPYDKLFNWNVDLKEKESLDLDQYPLGRKFLVQAGLRKRP 480
QY 446 FV-QAIAQCKHPPAPKEDDPLKKTFFWVNLKEKESLDLDQYPLGRKFLVQAGLRKRP 504
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 446 FV-QAIAQCKHPPAPKEDDPLKKTFFWVNLKEKESLDLDQYPLGRKFLVQAGLRKRP 504
QY 480 --TIGPRKRSAPSATSSKPAKR 500
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 480 --TIGPRKRSAPSATSSKPAKR 500
QY 505 KFTLGRKR-ATPTSSSTSTYAKR 526
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 505 KFTLGRKR-ATPTSSSTSTYAKR 526

```

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RESULT 8
US-09-991-053-1
; Sequence 1, Application US/09991053
; Publication No. US20030003532A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen
; APPLICANT: Chen, Xiaojiang
; TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
; TITLE OF INVENTION: virus
; FILE REFERENCE: Harvard/Harrison 12687/1120
; CURRENT APPLICATION NUMBER: US/09/991,053
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-18
; PRIOR APPLICATION NUMBER: 60/125208
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/148544
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-991-053-1

```

```

Query Match 65.9%; Score 1801; DB 11; Length 531;
Best Local Similarity 66.0%; Pred. No. 2,8e-177;
Matches 332; Conservative 69; Mismatches 96; Indels 6; Gaps 5;
QY 1 MALMRSDNTVYLPPEPSVAVVNTDDYRTSTIFYHAGSSRLTGVNPFYRVRVAGGNGK 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 MSMLPSEAVTVLPPEPSVAVVNTDDYRTSTIFYHAGSSRLTGVNPFYRVRVAGGNGK 60
QY 61 DLPKVSAYOYRFRVLOLDPNKGFLPDNSIYNFETORLWACAGVEIGRGQPLGVLGSH 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DLPKVSAYOYRFRVLOLDPNKGFLPDNSIYNFETORLWACAGVEIGRGQPLGVLGSH 120
QY 87 LVPKVSGLQYRFRVRLPDPNKGFPDTSFYDPAQRLWACAGVEIGRGQPLGVLGSH 146
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 87 LVPKVSGLQYRFRVRLPDPNKGFPDTSFYDPAQRLWACAGVEIGRGQPLGVLGSH 146
QY 121 PFYNTKDDTRESSHAATSNVSEYRDVNVSDYKOTQCLIGCAPAIGEHNAKGTACKSRPL 180
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 PFYNTKDDTRESSHAATSNVSEYRDVNVSDYKOTQCLIGCAPAIGEHNAKGTACKSRPL 180

```

```

Db 147 PLINKLDDTENASAVYAMGVNDRRECIISMDYKOTQCLIGCKPPIEBHMGKSPCTNVAV 206
QY 181 SOGDCPPELEKNTVLEDGDMVDVGYGAMDESTLQDCKCEVPLDICKOSICKYPPYLQMSAD 240
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 207 NPEDCCPELEKNTVLEDGDMVDVGYGAMDESTLQDCKCEVPLDICKOSICKYPPYLQMSAD 266
QY 241 PIGDSMFECILRRQLEFARHFNWAGMGDTVPQSLYIKGTGMARSPGSCVSPSPGSIY 300
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 PYGDSMFECILRRQLEFARHFNWAGMGDTVPQSLYIKGTGMARSPGSCVSPSPGSIY 300
QY 301 TSDSOLEFNKPYMLQKQGHNGICWGNOLFTVYVDDTRSTNLTICASTOSPVGQYDARK 360
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 TSDSOLEFNKPYMLQKQGHNGICWGNOLFTVYVDDTRSTNLTICASTOSPVGQYDARK 360
QY 361 FKQYSHREBYDQLEFQOLCTITLTDVMSYIHSNNSILEDNMFVGPPEPTSLVDYR 420
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 FKQYSHREBYDQLEFQOLCTITLTDVMSYIHSNNSILEDNMFVGPPEPTSLVDYR 420
QY 421 FVQSVATITQKDAAPAEKNDPYDKLFNWNVDLKEKESLDLDQYPLGRKFLVQAGLRKRP 479
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 FVQSVATITQKDAAPAEKNDPYDKLFNWNVDLKEKESLDLDQYPLGRKFLVQAGLRKRP 479
QY 446 FV-QAIAQCKHPPAPKEDDPLKKTFFWVNLKEKESLDLDQYPLGRKFLVQAGLRKRP 504
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 446 FV-QAIAQCKHPPAPKEDDPLKKTFFWVNLKEKESLDLDQYPLGRKFLVQAGLRKRP 504
QY 480 --TIGPRKRSAPSATSSKPAKR 500
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 480 --TIGPRKRSAPSATSSKPAKR 500
QY 505 KFTLGRKR-ATPTSSSTSTYAKR 526
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 505 KFTLGRKR-ATPTSSSTSTYAKR 526

```

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RESULT 9
US-10-301-260A-1
; Sequence 1, Application US/10301260A
; Publication No. US20030118609A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen
; APPLICANT: Chen, Xiaojiang
; TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
; TITLE OF INVENTION: virus
; FILE REFERENCE: Harvard/Harrison 12687/1123
; CURRENT APPLICATION NUMBER: US/10/301,260A
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 09/520,822
; PRIOR FILING DATE: 2000-03-18
; PRIOR APPLICATION NUMBER: 60/125208
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/148544
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-301-260A-1

```

```

Query Match 65.9%; Score 1801; DB 15; Length 531;
Best Local Similarity 66.0%; Pred. No. 2,8e-177;
Matches 332; Conservative 69; Mismatches 96; Indels 6; Gaps 5;
QY 1 MALMRSDNTVYLPPEPSVAVVNTDDYRTSTIFYHAGSSRLTGVNPFYRVRVAGGNGK 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 MSMLPSEAVTVLPPEPSVAVVNTDDYRTSTIFYHAGSSRLTGVNPFYRVRVAGGNGK 60
QY 61 DLPKVSAYOYRFRVLOLDPNKGFLPDNSIYNFETORLWACAGVEIGRGQPLGVLGSH 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DLPKVSAYOYRFRVLOLDPNKGFLPDNSIYNFETORLWACAGVEIGRGQPLGVLGSH 120
QY 87 LVPKVSGLQYRFRVRLPDPNKGFPDTSFYDPAQRLWACAGVEIGRGQPLGVLGSH 146
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 87 LVPKVSGLQYRFRVRLPDPNKGFPDTSFYDPAQRLWACAGVEIGRGQPLGVLGSH 146
QY 121 PFYNTKDDTRESSHAATSNVSEYRDVNVSDYKOTQCLIGCAPAIGEHNAKGTACKSRPL 180
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 PFYNTKDDTRESSHAATSNVSEYRDVNVSDYKOTQCLIGCAPAIGEHNAKGTACKSRPL 180
QY 147 PLINKLDDTENASAVYAMGVNDRRECIISMDYKOTQCLIGCKPPIEBHMGKSPCTNVAV 206
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 147 PLINKLDDTENASAVYAMGVNDRRECIISMDYKOTQCLIGCKPPIEBHMGKSPCTNVAV 206
QY 181 SOGDCPPELEKNTVLEDGDMVDVGYGAMDESTLQDCKCEVPLDICKOSICKYPPYLQMSAD 240
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 SOGDCPPELEKNTVLEDGDMVDVGYGAMDESTLQDCKCEVPLDICKOSICKYPPYLQMSAD 240
QY 207 NPEDCCPELEKNTVLEDGDMVDVGYGAMDESTLQDCKCEVPLDICKOSICKYPPYLQMSAD 266
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 207 NPEDCCPELEKNTVLEDGDMVDVGYGAMDESTLQDCKCEVPLDICKOSICKYPPYLQMSAD 266

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;
; LENGTH: 508 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1
US-09-822-662-1

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Query Match          48.5%; Score 1324.5; DB 10; Length 508;
Best Local Similarity 49.2%; Pred. No. 5,8e-128;
Matches 249; Conservative 88; Mismatches 158; Indels 11; Gaps 8;

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QY 1 MALMRSDNTVYLPPPSVARVNTDDYVTRTSIFYHAGSSRLLTGVPFRYPAGGANKQ 60
DB 7 MAVMLPAQNKFTYLPQPTIRLSTDEYSTRINLFYHATSERLLTVGHPEI--SSNOFY 64
QY 61 DIPKVAAYQYRVFVQVLPDPNKEGLPDNSIYNPEQRLVMACAGVITIGQPLGVLSGH 120
DB 65 TLPKVSFNAFRVRFVADPNRPAFGDKALFNPETRLVGLGIGRQPLGIGITGH 124
QY 121 PFYKRLDPTES--SHAATSNVSEEDVRDNVSVDYKQQLCTIGCAPAIGEHMAKGTACKSRP 179
DB 125 PLNKRKDDADENPTNYINTHANGDSRONTAFDAKQTMFLVGCIPASGEHNT--SRKCPGEQ 183
QY 180 LSGQDCPRLKNTVLEDDMDVDTGYGAMDFTLDPTKCEVPLDICSICKYPPDYLOMSA 239
DB 184 VKRGDCPRLVQIESVLEDDMDMDIGFAMDFALQODKSDVPLDVQATCKPYDIRMNH 243
QY 240 DPGVDSMEFCLREQGFARHFWRNACTMGD--TVPSQLYIKGTG--KRASGSCVYSPSPS 296
DB 244 EAVGNMFEFFARREQDQYTHFETRGSSVSDKEAVPQSLYLTADAPRTLATNTYVGTSPS 303
QY 297 GSIVTSDSOLFENKPYMLHKAQGNHNGICMNOLETVVDTTRSTNTLTCASQSPVPGQY 356
DB 304 GSNVSSDVQLEFNSTYLGQGGONNGIGNRNOLEFIVGDNTRGTSLSI--SMKNNASTTY 361
QY 357 DATKQYQSHVEEYVLOFTFLOCTTLTADVMSYHSNMSSTLEDNMFGVPPPTTSVLY 416
DB 362 SNANFDFLRHTEEFLEFIVQLCKVLTPENLAYIHTMDPNILEDNMOLSVSQPPIPLE 421
QY 417 DRYRFV--QSVATVTCQDAAPAENKDPYDLKFMNVDLKEKFSLDLDOYRGRRELVQAGL 475
DB 422 DQRFAGSSLAACPDQAPPEPOTDPSQKFEVVDLTERMSQDLPFLGRKFLYQSGM 481
QY 476 -RRKPTIGPRKRSAPSATTSKPKAKR 500
DB 482 TORRATSSTTKRTVAVSTSAKRRK 507

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RESULT 12

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US-09-134-377-2
; Sequence 2, Application US/09134377
; Patent No. US20020015710A1
; GENERAL INFORMATION:
; APPLICANT: SCHLEGEL, C. Richard
; APPLICANT: JENSON, A. Bennett
; APPLICANT: GHIM, Shin-Je
; TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134, 377

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/724, 281
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 010091-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-134-377-2

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```

Query Match          47.5%; Score 1298; DB 9; Length 503;
Best Local Similarity 48.2%; Pred. No. 3.2e-125;
Matches 247; Conservative 92; Mismatches 153; Indels 20; Gaps 8;

```

```

QY 1 MALMRSDNTVYLPPPSVARVNTDDYVTRTSIFYHAGSSRLLTGVPFRYPAGGANKQ 60
DB 1 MAVMLPAQNKFTYLPQPTIRLSTDEYSTRINLFYHATSERLLTVGHPEI-----YKE 55
QY 61 D-----IPKVAAYQYRVFVQVLPDPNKEGLPDNSIYNPEQRLVMACAGVEIGRQPLG 114
DB 56 ERSEEVIVPKEVSPNOQYRVEFLRLPDPNNFAGDKSLFDPKEKRLVGLRGLFEGROPYG 115
QY 115 VGSIGHPYKLDDE--SSHAATSNVSEEDVRDNVSVDYKQQLCTIGCAPAIGEHMAK 172
DB 116 ISYGHPTEDRYNDVDPNKNLHAGGGTDSRVNMGIDPRQOTQMFHIGCKPALGESHSLT 175
QY 173 TACKSRPLSGQDCPRLKNTVLEDDMDVDTGYGAMDFTLDPTKCEVPLDICSICKYR 232
DB 176 RMCTGVNHTAGQCPRIELRNTTIEDGMDVIGFAMDFALQYHKGSGVPLDIYNSAKTP 235
QY 233 DYLOMSADPYGDSMEFCLREQGFARHFWRNACTMGD--TVPSQLYIKGTGMRASPGSCVY 291
DB 236 DYLMANEPYEDCFEFVREQLYARHINSRSGTGLEVPKDY--ATREDNNIGTNY 293
QY 292 SPSPSGSIYSDSOLFENKPYMLHKAQGNHNGICMNOLETVVDTTRSTNTLTCASQ--S 350
DB 294 FSTPSSGLVSSGOLNRPYWIORSOGKNGIAMGNOLFTVVDTRGTPLTINIGQDOK 353
QY 351 PVBQYDATKQYSHVEEYDLOFTFLOCTTLTADVMSYHSNMSSTLEDNMFGVPP 410
DB 354 PEGGNVYPSRYRRLRVEEYVSIYQLCKVLTSENLAIHTMDPNILEDNMHLVTPR 413
QY 411 PITSVDYTRFVQSVATVTCQDAAPAENKDPYDLKFMNVDLKEKFSLDLDOYRGRKEL 470
DB 414 SGT-LDDYTRYINSLTKPTNIPKTNVDPDFEFVVDLDMKTEQLDQPLGRKFL 472
QY 471 VQAGLRKPTIGPRKRSAPSATTSKPKAKR 502
DB 473 FQTNVLRKRSV--KVRSTSHSVYKRAVKKR 502

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RESULT 13

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US-09-822-662-2
; Sequence 2, Application US/09822662
; Publication No. US20020197264A1
; GENERAL INFORMATION:
; APPLICANT: SCHLEGEL, C. Richard
; APPLICANT: JENSON, A. Bennett
; APPLICANT: GHIM, Shin-Je
; TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:

```

```

ADDRESS: BURNS, DOANE, SNECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22131-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/822,662
FILING DATE: 02-Apr-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/724,281
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 010091-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-822-662-2

Query Match      47.5%; Score 1298; DB 10; Length 503;
Best Local Similarity 48.2%; Pred. No. 3.2e-125;
Matches 247; Conservative 92; Mismatches 153; Indels 20; Gaps 8;

OY 1 MALMRPSDNTVYLLPPPSVARYNTDDYVTRTSIFYHAGSSRLTLVGNPFYRPVAGGNGKQ 60
DB 1 MAVMLPQNKRYLLPQSTKVLSTDEVYSRTNIFYHASSERLLTVGHFYEI-----YKE 55
OY 61 D-----IPKSAOYRFRVQLPDPNKGFLPDNSIYNPFTQRLVMACAGVEIGRGQPLG 114
DB 56 ERSEVATYPKVSPNOYRFRLLPDPNNEAFGDSLEPPEKERLVMGLRGLEIGRGQPLG 115
OY 115 VGLSGHPYKRLDTE--SSHAATSNVSEVDYRVNVDYKOTQCLIGCAPAIGHMAKG 172
DB 116 ISVIGHPTFDYRNVENENKMLAGHGSGTDSRVNMGGLDPKOTQFMIGCKRALKGHSGLT 175
OY 173 TACKSRPLSGDCRPLELKNLTVEGDVNTGYGAMDFSTLDTKCEVPLDICOISICKYR 232
DB 176 RMCGOVHTAGQCPRLELNTTIEDGMVDIGFGAMDFKALQHYKSGVPIDIVSACKYR 235
OY 233 DYLMSADPYGDSMFCRLRROLFARHFWNRAGTMG-DTVPOSILYIKGTGRASPGSCVY 291
DB 236 DYLMAANPEYGRCEFFVRRLQYLARHMSRSGTGLEPVPKDY--ATREDNNIGTNY 293
OY 292 SPSPSGSIVTSDOLFENKPYMLHKAQGNHNCICWHNOLFVTVVDTTRSTNLTICASTQ-S 350
DB 294 FSTISGSLVSSGQLFNRPTIORSQGNNGIANGNOLFVTVVDTTRSTNLTICASTQ-S 353
OY 351 PVPQOYATKPKQSRHYEEDLOFIFOLCTITTLADVMSYIHSNNSILEDWNGVPPPTSLVD 410
DB 354 PEEGNVYVSSRYTLRHYEEYVSIYQLCKVKLSPEMLALIHMDPIIIDMHNATYRPP 413
OY 411 PTTSLVDTYRVOYATTCQDAAPAEKNDPYDKLKEWNVLDLKEKFSJLDLQYLGKREL 470
DB 414 SGT-LDDTYRYINSLATCPTNIPKTVNDPFRDKEWEVDLKDMLQDTPLGKREL 472
OY 471 VQAGIRKRPITGPRKRSAPSATSSKPAKRYR 502

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DB 473 FQINVLRRSV--KVNSTSHVSKRAVKRRR 502

RESULT 14
US-10-305-765-2
Sequence 2, Application US/10305765
Publication No. US20030175907A1
GENERAL INFORMATION:
APPLICANT: FRAZER, Ian Hector
APPLICANT: ZHOU, Jian
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AND METHOD FOR SELECTIVELY
FILE REFERENCE: 210338.0001/1US
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: US/10/305,765
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: PCT/AU98/00530
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: AU P07765
PRIOR FILING DATE: 1997-07-09
PRIOR APPLICATION NUMBER: AU P09467
PRIOR FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 219
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 495
TYPE: PRT
ORGANISM: Bovine papillomavirus type 1
FEATURE:
OTHER INFORMATION: LI open reading frame (wild-type)
US-10-305-765-2

Query Match      46.9%; Score 1283; DB 12; Length 495;
Best Local Similarity 48.3%; Pred. No. 1.1e-123;
Matches 243; Conservative 90; Mismatches 156; Indels 14; Gaps 7;

OY 1 MALMRPSDNTVYLLPPPSVARYNTDDYVTRTSIFYHAGSSRLTLVGNPFYRPVAGGNGKQ 60
DB 1 MALMOQCGK-LYLPPTPVSKVLCSEYVQKRSIFYHETERLLTIGHYPVVSIGA--K 56
OY 61 DIPKSAOYRFRVQLPDPNKGFLPDNSIYNPFTQRLVMACAGVEIGRGQPLG 120
DB 57 TVPKVSAOYRFRVQLPDPNKGFLPDNSIYNPFTQRLVMACAGVEIGRGQPLG 116
OY 121 PFYKRLDTESSHAATSNVSEVDYRVNVDYKOTQCLIGCAPAIGHMAKGTAACKSRPL 180
DB 117 PTFNALDAENRVNKKVTTQTDDRKQGLGAKQOQIILLGOTPAEGEYWTARPCVTDR 176
OY 181 SGGCPRLELKNLTVEGDVNTGYGAMDFSTLDTKCEVPLDICOISICKYRPTQLMSAD 240
DB 177 ENGACPRLELKNKIEEDGDMIEIGFANFEKINASDPLDIONEICLYPDILKNAED 236
OY 241 PYGSMFECRLRROLFARHFWNRAGTMGDVPOSILYI--KGTGMRASPGSCVYSPSPSG 297
DB 237 AAGSMFEPFAKKEVYRHRHITRKGSSEKAPTTFTYKNNKGADTLKTPS--VHFGSPSG 294
OY 298 SIYVSDSOLFENKPYMLHKAQGNHNCICWHNOLFVTVVDTTRSTNLTICASTQSPVPCOYD 357
DB 295 SLVSTDNQIENRPTIORSQGNNGIANGNOLFVTVVDTTRSTNLTICASTQSPVPCOYD 354
OY 358 ATKPKOYSRHYEEDLOFIFOLCTITTLADVMSYIHSNNSILEDWNGVPPPTSLVD 417
DB 355 SSKFNVYRHRHEEYKLIETLCSEVETAGVSHLQGLMPSYLENWEIGVQPPSSILED 414
OY 418 TYRVOYATTCQDAAPAEKNDPYDKLKEWNVLDLKEKFSJLDLQYLGKREL 477
DB 415 TYRIESPATKCAVNPAPK-EDPYAGKFWNIDLKELSLDLOFPLGRFLAQOAGGC 473
OY 478 KPTIGPRKRSAPSATSSKPAKRYR 500
DB 474 STV---KKRRI-SQKTSKPAKK 492

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RESULT 15
US-10-305-765-4
; Sequence 4, Application US/10305765
; Publication No. US20030175907A1
; GENERAL INFORMATION:
; APPLICANT: FRAZER, Ian Hector
; APPLICANT: ZHOU, Jian
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AND METHOD FOR SELECTIVELY
; TITLE OF INVENTION: EXPRESSING A PROTEIN IN A TARGET CELL OR TISSUE
; FILE REFERENCE: 210338.0001/1US
; CURRENT APPLICATION NUMBER: US/10/305,765
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US/09/479, 645
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: PCT/AU98/00530
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: AU P07765
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: AU P09467
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bovine
; OTHER INFORMATION: papillomavirus type 1 L1 open reading frame
; FEATURE:
; OTHER INFORMATION: (humanized)
; OTHER INFORMATION: wild-type codons replaced with synonymous codons
; OTHER INFORMATION: used at relatively high frequency by human genes
US-10-305-765-4

Query Match 46.9%; Score 1283; DB 12; Length 495;

Best Local Similarity 48.3%; Pred.No. 1.1e-123;

Matches 243; Conservative 90; Mismatches 156; Indels 14; Gaps 7;

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QY      1 MALMPSPDWTYVLPSPSVARVNTDDYVTRTSIFYHAGSSRLTLVGNPFYFRYPAGGNKO 60
DB      1 MALMOOGOK-LYLPPTPSKVCSEYVQKRSIFTHAETERLLTIGHPTVPVSGA--K 56
QY      61 DIPKVSAYQYRVFVQLDPNKFGLPDSINYPETQRLVMACAGVEIGRQPLGVGLSGH 120
DB      57 TVPKVSANQYRVFKIQLPDNPQFALPDRVHNPSKERLWPIGVVSRGQPLGTVTGH 116
QY      121 PPKNLDTESHAATSNSEVDYRNVSYDKOTQLCITGCAPIGEMHAKGTACKSRPL 180
DB      117 PTFNALDLAENVNRKVTQTQTDKQOTGIDAKOOIILLGCTPAEGEYWTARPCVTDRL 176
QY      181 SGGDPPLELKNVTLEDGMDVDTGYGAMDFSLDQPKCEVPLDQICOSTCKYDPDYLOMSAD 240
DB      177 ENGACPPLELKNKHIEDGDMETIGGAAFEKINASKSDPLDQNEICLYPDYLMMAED 236
QY      241 PYGDSMFFCLRRQQLFARHFNRACTMGTPVQSLYI--KGTGMRASPSGCVSPSPSG 297
DB      237 AAGNSMFFPARKEQYVRIWIRGSEKAPPTDIFYLKNKGDATLKLPS--VHGSPPSG 294
QY      298 SLVTSDSQLFNKPYVLHKAQGHNGICWHNQLFTVVDTRSTNLTICASTQSPVPGQYD 357
DB      295 SLVSTDNQIFNRPYMLFRAQGMNNGIAWNNILFLTVGDNTRGTNLTISVASDGTPLTEYD 354
QY      358 ATKFKQYSRHVEYDLOFLOCTITLADVMYSIHMSNSTLEDMNFQVPPPTSLVD 417
DB      355 SKSENVYHRHMEYKLAFTLELCSVETIAQTIVSHLQGLMPSVLENMEIGVQPTTSILED 414
QY      418 TTRFYQVAITQCKDAPEAKNDPYDKLFMNVVDLKEKFSLDQYPLGRKFLVQAGLR 477
DB      415 TYRTIESPATKCAENVIPAK-EDPYAGCFEWMNIDLEKSLDLDQPLGRRLAQQAGAC 473
QY      478 KPTIGPKRRKSPASNTSSKPAKR 500
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DB 474 STV---RKRRI-SQRTSSKPAKR 492

Search completed: October 17, 2003, 11:15:36
Job time : 49.6622 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 17, 2003, 10:57:04 ; Search time 22.5217 Seconds
(without alignments)
952,486 Million cell updates/sec

Title: US-08-913-644-2

Perfect score: 2733
Sequence: 1 MALMRPSDNTVYLPSPSVAR.....APSATTSSKPAKRVRRANK 507

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2733	100.0	507	2	US-08-409-122-2
2	2733	100.0	507	2	US-08-408-669-2
3	2705	99.0	568	4	US-09-520-822A-3
4	1826	66.8	505	3	US-08-920-822A-3
5	1826	66.8	505	4	US-08-944-368A-2
6	1826	66.8	505	4	US-09-820-764-2
7	1801	65.9	531	4	US-09-986-118A-2
8	1789.5	65.5	497	4	US-09-520-822A-1
9	1789.5	65.5	499	4	US-09-413-611A-6
10	1768.5	64.7	532	3	US-08-737-336-6
11	1742.5	63.8	500	2	US-08-987-519-1
12	1726.5	63.2	501	2	US-08-987-519-1
13	1679	61.4	501	2	US-08-987-519-3
14	1324.5	48.5	508	2	US-08-724-281-1
15	1324.5	48.5	508	4	US-09-134-377-1
16	1298	47.5	503	2	US-08-724-281-2
17	1298	47.5	503	4	US-09-134-377-2
18	1283	46.9	495	4	US-09-479-645A-4
19	1283	46.9	495	4	US-09-479-645A-2
20	1271	46.5	964	4	US-08-484-791-2
21	604	22.1	132	4	US-09-000-266-29
22	604	22.1	132	4	US-09-628-099-29
23	604	22.1	132	4	US-10-056-360-29
24	604	22.1	132	4	US-10-056-359-29
25	510	18.7	128	4	US-09-319-056B-14
26	493	18.0	128	4	US-09-319-056B-17
27	487.5	17.8	127	4	US-09-319-056B-11

28	423.5	15.5	145	4	US-09-485-973-10	Sequence 10, Appl
29	396	14.5	136	4	US-09-319-056B-8	Sequence 8, Appl
30	382.5	14.0	131	4	US-09-319-056B-23	Sequence 23, Appl
31	379.5	13.9	145	4	US-09-485-973-8	Sequence 8, Appl
32	374	13.7	144	4	US-09-000-266-5	Sequence 5, Appl
33	374	13.7	144	4	US-09-628-099-5	Sequence 5, Appl
34	374	13.7	144	4	US-10-056-360-5	Sequence 5, Appl
35	374	13.7	144	4	US-10-056-359-5	Sequence 5, Appl
36	367	13.4	128	4	US-09-319-056B-5	Sequence 5, Appl
37	363	13.3	136	4	US-09-000-266-8	Sequence 8, Appl
38	363	13.3	136	4	US-09-628-099-8	Sequence 8, Appl
39	363	13.3	136	4	US-10-056-360-8	Sequence 8, Appl
40	363	13.3	136	4	US-10-056-359-8	Sequence 8, Appl
41	359.5	13.2	139	4	US-09-319-056B-2	Sequence 2, Appl
42	359.5	13.2	139	4	US-09-000-266-2	Sequence 2, Appl
43	359.5	13.2	139	4	US-09-628-099-2	Sequence 2, Appl
44	359.5	13.2	139	4	US-10-056-360-2	Sequence 2, Appl
45	359.5	13.2	139	4	US-10-056-359-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-409-122-2, Application US/08409122

Patent No. 5820870

GENERAL INFORMATION:

APPLICANT: JOYCE, JAMES G.

APPLICANT: GEORGE, HUGH A.

APPLICANT: HOFMANN, KATHRYN J.

APPLICANT: JANSSEN, KATHRYN U.

APPLICANT: NEESPER, MICHAEL P.

TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE 18 VACCINE

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHRISTINE E. CARTY - MERCK & CO., INC.

STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000

CITY: RAHWAY

STATE: NJ

COUNTRY: US

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/409,122

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/408,669

FILING DATE: 22-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: CARTY, CHRISTINE E

REGISTRATION NUMBER: 36,099

REFERENCE/DOCKET NUMBER: 19425

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-594-6734

TELEFAX: 908-594-4720

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 507 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

US-08-409-122-2

Query Match 100.0%; Score 2733; DB 2; Length 507;
 Best Local Similarity 100.0%; Pred. No. 2, 2e-278;
 Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MALMRPSDNTVYLPPEPVAVRVNTDQVYTRTSIFYHAGSSRLTLVGNPFYRVPGGKQ 60
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DB 1 MALMRPSDNTVYLPPEPVAVRVNTDQVYTRTSIFYHAGSSRLTLVGNPFYRVPGGKQ 60
QY 61 DIPKVSAYQYRVFVQVLPDPNKKFGLPDNSIYNPETORLVWACAGVEIGRQPLGVLSGH 120
  |||||||
DB 61 DIPKVSAYQYRVFVQVLPDPNKKFGLPDNSIYNPETORLVWACAGVEIGRQPLGVLSGH 120
QY 121 PFYVKLDDTSSHAATSNVEDVDVNSVDYKQTOCLILCAPAIGEHMAKGTACKSRPL 180
  |||||||
DB 121 PFYVKLDDTSSHAATSNVEDVDVNSVDYKQTOCLILCAPAIGEHMAKGTACKSRPL 180
QY 181 SGGCCPPELEKNTVLEGGDMVDYGYGAMDFSTLQDTCCEVPLDLCOSICKYPPYLQMSAD 240
  |||||||
DB 181 SGGCCPPELEKNTVLEGGDMVDYGYGAMDFSTLQDTCCEVPLDLCOSICKYPPYLQMSAD 240
QY 241 PYGDSMFECFLRREQLFARHFMNRRAGTMDGVYPOSILYKGTGMRASPGSCYSPSPSGSIY 300
  |||||||
DB 241 PYGDSMFECFLRREQLFARHFMNRRAGTMDGVYPOSILYKGTGMRASPGSCYSPSPSGSIY 300
QY 301 TSDSQLEFNKPYWLHKAGGHNNGICWNNQLEFVTVVDTTRSTNLITICASTQSPVPGQYDATK 360
  |||||||
DB 301 TSDSQLEFNKPYWLHKAGGHNNGICWNNQLEFVTVVDTTRSTNLITICASTQSPVPGQYDATK 360
QY 361 FKQSRHVEEYDLOFIQOLCTITLTADVMSTIHSNSSLIEDMNFQVPPPTTSLVDTYR 420
  |||||||
DB 361 FKQSRHVEEYDLOFIQOLCTITLTADVMSTIHSNSSLIEDMNFQVPPPTTSLVDTYR 420
QY 421 FVQSVATTCQKDAAPAKNKPYDLKRFWNVDLKEKFSILDQYPLGKKFLVQAGLRKRP 480
  |||||||
DB 421 FVQSVATTCQKDAAPAKNKPYDLKRFWNVDLKEKFSILDQYPLGKKFLVQAGLRKRP 480
QY 481 IGPKRSPASATTSKPAKRVYRARK 507
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DB 481 IGPKRSPASATTSKPAKRVYRARK 507

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RESULT 2

US-08-408-669-2

; Sequence 2, Application US/08408669
 ; Patent No. 5840306

; GENERAL INFORMATION:

; APPLICANT: JOHANN, KATHRYN J.

; APPLICANT: NEER, MICHAEL P.

; TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE 18

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000

; CITY: RAHWAY

; STATE: NJ

; COUNTRY: US

; ZIP: 07065-0907

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; FILING DATE: 22-MAR-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

NAME: CARTY, CHRISTINE E
 REGISTRATION NUMBER: 36,099
 REFERENCE/DOCKET NUMBER: 19424
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-594-6734
 TELEFAX: 908-594-4720
 TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 507 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

US-08-408-669-2

Query Match 100.0%; Score 2733; DB 2; Length 507;
 Best Local Similarity 100.0%; Pred. No. 2, 2e-278;
 Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MALMRPSDNTVYLPPEPVAVRVNTDQVYTRTSIFYHAGSSRLTLVGNPFYRVPGGKQ 60
  |||||||
DB 1 MALMRPSDNTVYLPPEPVAVRVNTDQVYTRTSIFYHAGSSRLTLVGNPFYRVPGGKQ 60
QY 61 DIPKVSAYQYRVFVQVLPDPNKKFGLPDNSIYNPETORLVWACAGVEIGRQPLGVLSGH 120
  |||||||
DB 61 DIPKVSAYQYRVFVQVLPDPNKKFGLPDNSIYNPETORLVWACAGVEIGRQPLGVLSGH 120
QY 121 PFYVKLDDTSSHAATSNVEDVDVNSVDYKQTOCLILCAPAIGEHMAKGTACKSRPL 180
  |||||||
DB 121 PFYVKLDDTSSHAATSNVEDVDVNSVDYKQTOCLILCAPAIGEHMAKGTACKSRPL 180
QY 181 SGGCCPPELEKNTVLEGGDMVDYGYGAMDFSTLQDTCCEVPLDLCOSICKYPPYLQMSAD 240
  |||||||
DB 181 SGGCCPPELEKNTVLEGGDMVDYGYGAMDFSTLQDTCCEVPLDLCOSICKYPPYLQMSAD 240
QY 241 PYGDSMFECFLRREQLFARHFMNRRAGTMDGVYPOSILYKGTGMRASPGSCYSPSPSGSIY 300
  |||||||
DB 241 PYGDSMFECFLRREQLFARHFMNRRAGTMDGVYPOSILYKGTGMRASPGSCYSPSPSGSIY 300
QY 301 TSDSQLEFNKPYWLHKAGGHNNGICWNNQLEFVTVVDTTRSTNLITICASTQSPVPGQYDATK 360
  |||||||
DB 301 TSDSQLEFNKPYWLHKAGGHNNGICWNNQLEFVTVVDTTRSTNLITICASTQSPVPGQYDATK 360
QY 361 FKQSRHVEEYDLOFIQOLCTITLTADVMSTIHSNSSLIEDMNFQVPPPTTSLVDTYR 420
  |||||||
DB 361 FKQSRHVEEYDLOFIQOLCTITLTADVMSTIHSNSSLIEDMNFQVPPPTTSLVDTYR 420
QY 421 FVQSVATTCQKDAAPAKNKPYDLKRFWNVDLKEKFSILDQYPLGKKFLVQAGLRKRP 480
  |||||||
DB 421 FVQSVATTCQKDAAPAKNKPYDLKRFWNVDLKEKFSILDQYPLGKKFLVQAGLRKRP 480
QY 481 IGPKRSPASATTSKPAKRVYRARK 507
  |||||||
DB 481 IGPKRSPASATTSKPAKRVYRARK 507

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RESULT 3

US-09-520-822A-3

; Sequence 3, Application US/09520822A
 ; Patent No. 6551597

; GENERAL INFORMATION:

; APPLICANT: Harrison, Stephen

; APPLICANT: Chen, Xiaojiang

; TITLE OF INVENTION: Vaccine compositions and methods for human papilloma

; TITLE OF INVENTION: virus

; FILE REFERENCE: Harvard/Harrison 12687/1120

; CURRENT APPLICATION NUMBER: US/09/520,822A

; CURRENT FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/125208
 ; PRIOR FILING DATE: 1999-03-18
 ; PRIOR APPLICATION NUMBER: 60/148544
 ; PRIOR FILING DATE: 1999-08-12
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 568
 ; TYPE: PR1
 ; ORGANISM: Human papillomavirus type 18
 US-09-520-822A-3

Query Match 99.0%; Score 2705; DB 4; Length 568;
 Best Local Similarity 99.0%; Pred. No. 2,3e-275;
 Matches 502; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MALMRSDNTVYLPSPSVARVNTDDYVRTSTIFYHAGSSRLTGVNPPYRVAGGNKQ 60
 DB 62 MALMRSDNTVYLPSPSVARVNTDDYVRTSTIFYHAGSSRLTGVNPPYRVAGGNKQ 121
 QY 61 DIPKVSAYOYRVFRVOLPDPNKEGLPDNSIYNPETORLVACAGVEIGRGQPLGVLSGH 120
 DB 122 DIPKVSAYOYRVFRVOLPDPNKEGLPDSTIYNPETORLVACAGVEIGRGQPLGVLSGH 181
 QY 121 PFYNKLDDESSHAATSNVSEVDYRVNVDYKOTQCLIGCAPAIGEHMAKGTACKSRPL 180
 DB 182 PFYNKLDDESSHAATSNVSEVDYRVNVDYKOTQCLIGCAPAIGEHMAKGTACKSRPL 241
 QY 181 SOGDCEPLELKNVLEDDGMVDVGYGAMDESTIADTKCEVPLDICSICKYPPYLQMSAD 240
 DB 242 SOGDCEPLELKNVLEDDGMVDVGYGAMDESTIADTKCEVPLDICSICKYPPYLQMSAD 301
 QY 241 PYGDSMEFCLRRQLEFARHFNWAGTMDTPVPSLYIKGTGRASPGSCYSPSPSGSIY 300
 DB 302 PYGDSMEFCLRRQLEFARHFNWAGTMDTPVPSLYIKGTGRASPGSCYSPSPSGSIY 361
 QY 301 TTSOQLFNKPYWHLKQGHNGICWNNOLFVTVVDTTRSTNLTCASSTOSPVGOYDARK 360
 DB 362 TTSOQLFNKPYWHLKQGHNGICWNNOLFVTVVDTTRSTNLTCASSTOSPVGOYDARK 421
 QY 361 FKOYSRHVEEYDLOFIFOLCTITLTADVMSYIHSNMSILEDNFGVPPPTSLVDYR 420
 DB 422 FKOYSRHVEEYDLOFIFOLCTITLTADVMSYIHSNMSILEDNFGVPPPTSLVDYR 481
 QY 421 FVOSVAITCOKDAAPAKNDPYDKLKFVNVDLKEKESLDLDQYPLGRKFLVQAGLRKRP 480
 DB 482 FVOSVAITCOKDAAPAKNDPYDKLKFVNVDLKEKESLDLDQYPLGRKFLVQAGLRKRP 541
 QY 481 IGPKRKSAPSATSSKPAKRVRRARK 507
 DB 542 IGPKRKSAPSATSSKPAKRVRRARK 568

RESULT 4
 US-08-944-368A-2
 ; Sequence 2, Application US/08944368A
 ; Patent No. 6228368
 ; GENERAL INFORMATION:
 ; APPLICANT: Glasman, et al.
 ; TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
 ; TITLE OF INVENTION: Formulations and Methods of Use
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; STREET: 233 South Wacker Drive, 6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/944,368A
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Williams Jr., Joseph A.
 ; REGISTRATION NUMBER: 38,659
 ; REFERENCE/DOCKET NUMBER: 27013/34028
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; TELEFAX: 312-474-0448
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 505 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-944-368A-2

Query Match 66.8%; Score 1826; DB 3; Length 505;
 Best Local Similarity 66.3%; Pred. No. 5e-183;
 Matches 333; Conservative 68; Mismatches 97; Indels 4; Gaps 3;

QY 1 MALMRSDNTVYLPSPSVARVNTDDYVRTSTIFYHAGSSRLTGVNPPYRVAGGNKQ 60
 DB 1 MSMLRSEATVYLPSPSVARVNTDEYVANTINIFYHAGSRLAVGHPIPKNNKTI 60
 QY 61 DIPKVSAYOYRVFRVOLPDPNKEGLPDNSIYNPETORLVACAGVEIGRGQPLGVLSGH 120
 DB 61 LVPKVSGLOYRVFRHILPDPNKEGFPDTSFYNDPQRLVACAGVEIGRGQPLGVLSGH 120
 QY 121 PFYNKLDDESSHAATSNVSEVDYRVNVDYKOTQCLIGCAPAIGEHMAKGTACKSRPL 180
 DB 121 PLNKLDDTENASAVIANNACVDRNRECIISMDYKOTQCLIGCKPIEBHMGKSPCTNVAY 180
 QY 181 SOGDCEPLELKNVLEDDGMVDVGYGAMDESTIADTKCEVPLDICSICKYPPYLQMSAD 240
 DB 181 NPDCPEPLELINVIVDGDMDVDTGFAMDTTIOAKSEVPLDICSICKYPPYIMVSE 240
 QY 241 PYGDSMEFCLRRQLEFARHFNWAGTMDTPVPSLYIKGTGRASPGSCYSPSPSGSIY 300
 DB 241 PYGDSMEFCLRRQLEFARHFNWAGTMDTPVPSLYIKGTGRASPGSCYSPSPSGSIY 300
 QY 301 TTSOQLFNKPYWHLKQGHNGICWNNOLFVTVVDTTRSTNLTCASSTOSPVGOYDARK 360
 DB 301 TSDQILFNKPYWHLKQGHNGICWNNOLFVTVVDTTRSTNMSLCAAI-STSETTYKNTN 359
 QY 361 FKOYSRHVEEYDLOFIFOLCTITLTADVMSYIHSNMSILEDNFGVPPPTSLVDYR 420
 DB 360 FKEYLRHGEYDLOFIFOLCTITLTADVMSYIHSNMSILEDNFGVPPPTSLVDYR 419
 QY 421 FVOSVAITCOKDAAPAKNDPYDKLKFVNVDLKEKESLDLDQYPLGRKFLVQAGLRKRP 479
 DB 420 FVTSOAIACQKHPTPAKEDPLEKKYFEWNLKEKESADLDQYPLGRKFLVQAGLRKRP 479
 QY 480 -TIGPKRKSAPSATSSKPAKRVRRARK 500
 DB 480 FTLGKRR-ATPTTSTSTAKR 500

RESULT 5
 US-09-820-764-2
 ; Sequence 2, Application US/09820764
 ; Patent No. 635266
 ; GENERAL INFORMATION:
 ; APPLICANT: BURGER, Alexander
 ; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
 ; TITLE OF INVENTION: FORMULATIONS AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESSES:


```
Db 301 TSDAQIFNKPFWLQRAQGHNNICGNQLFVTVDTTRSTNLSICAAI-STSETTYKNTN 359
Qy 361 FKQYRHHVEYDLOEITFOLCTITLADVMSYIHSNNSSILEDWNGVPPPTSLVDIYR 420
Db 360 FKEXLRHGEYDLOEITFOLCKITTLADVMTYIHSNNSTILEDWNGLOPPPGTLEDIYR 419
Qy 421 FVQSVAITCOKDAAPAEKNDPDKLFKFWNDLKEKFSLDLQDPYGRKFLVAGLRKRP- 479
Db 420 FVTSQAICQKHPPAPKEDDPLKKTFWENVLKEKFSADLDQPLGRKFLQAGLRKRP 479
Qy 480 -TIGPKRSAPSATTSSPKAR 500
Db 480 FTLGKRRK-ATPTTSSSTTAKR 500

RESULT 7
US-09-520-822A-1
; Sequence 1, Application US/09520822A
; Patent No. 6551597
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen
; APPLICANT: Chen, Xiaojiang
; TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
; FILE REFERENCE: Harvard/Harrison 12687/1120
; CURRENT APPLICATION NUMBER: US/09/520/822A
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/125208
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/148544
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-520-822A-1

Query Match
Best Local Similarity 65.9%; Score 1801; DB 4; Length 531;
Matches 332; Conservative 69; Mismatches 96; Indels 6; Gaps 5;

Qy 1 MALMRPSDNTVYLPPPSARVYNTDDYRTSIFYHAGSSRLITVGNPFYRPAAGGNKQ 60
Db 27 MSMLPSEATVYLPVPVSKVSTDEYVARTINITYHAGSRLLAVGHPPIKKNNNKI 86
Qy 61 DIPKSAVQYRFRQLDPNKEGLPDNSIVPEQORLVMACAGVEIGRQPLVGLSGH 120
Db 87 LVPKVSGLQYRFRHLDPNKEGFPDTSFYNPDRQLVMACVGEVGGQPLVGLSGH 146
Qy 121 PFYNNKLDTESSHAATSNVEDYRDVSVYKOTQCLICGAPAIGEHNAKGTACKSRPL 180
Db 147 PLNKLDDTEENASAAANAGVNRRCISMDYKOTQCLICGKRPPIGEHNGKSPCTNAY 206
Qy 181 SOGDCPPELKNVTYLEDGDMVDYTGAMDFSTLDTKCEVPLDIOQSTICKYDYIOMSD 240
Db 207 NPGDCPPELINTVYIDQDMVDTFGAMDFTLLQANKSEVPLDICTSICKYDYIKMSE 266
Qy 241 PYGDSMFCLREOLFARHFWNRAGTMDYVPOSLYIKGTGRASPGSCVYSPSGSIV 300
Db 267 PYGDSLFYLRBOHFVRHLFRKACTGVBVDDIYIKGSGSTANLASNFPPTSGSMV 326
Qy 301 TSDQOLFKNPYWLAKRQGHNNICGNQLFVTVVDTTRSTNLTICASTQSPYPGYDATK 360
Db 327 TSDAQIFNKPFWLQRAQGHNNICGNQLFVTVVDTTRSTNLSICAAI-STSETTYKNTN 385
Qy 361 FKQYRHHVEYDLOEITFOLCTITLADVMSYIHSNNSSILEDWNGVPPPTSLVDIYR 420
Db 360 FKEXLRHGEYDLOEITFOLCKITTLADVMTYIHSNNSTILEDWNGLOPPPGTLEDIYR 445
Qy 421 FVQSVAITCOKDAAPAEKNDPDKLFKFWNDLKEKFSLDLQDPYGRKFLVAGLRKRP 479
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Db 446 FV-TQAIACQKHPPAPKEDDPLKKTFWENVLKEKFSADLDQPLGRKFLQAGLRKRP 504
Qy 480 -TIGPKRSAPSATTSSPKAR 500
Db 505 KFTLGKRRK-ATPTTSSSTTAKR 526

RESULT 8
US-09-413-611A-6
; Sequence 6, Application US/09413611A
; Patent No. 6380364
; GENERAL INFORMATION:
; APPLICANT: Mueller, Martin
; APPLICANT: Kast, Wilbe
; APPLICANT: Nieland, John
; APPLICANT: Velders, Markwin
; TITLE OF INVENTION: Chimeric Biotin-Binding Papillomavirus Protein
; FILE REFERENCE: 202325
; CURRENT APPLICATION NUMBER: US/09/413/611A
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 60/109,510
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:biotin-binding
US-09-413-611A-6

Query Match
Best Local Similarity 65.5%; Score 1789.5; DB 4; Length 497;
Matches 325; Conservative 63; Mismatches 93; Indels 3; Gaps 2;

Qy 1 MALMRPSDNTVYLPPPSARVYNTDDYRTSIFYHAGSSRLITVGNPFYRPAAGGNKQ 60
Db 1 MSMLPSEATVYLPVPVSKVSTDEYVARTINITYHAGSRLLAVGHPPIKKNNNKI 60
Qy 61 DIPKSAVQYRFRQLDPNKEGLPDNSIVPEQORLVMACAGVEIGRQPLVGLSGH 120
Db 61 LVPKVSGLQYRFRHLDPNKEGFPDTSFYNPDRQLVMACVGEVGGQPLVGLSGH 120
Qy 121 PFYNNKLDTESSHAATSNVEDYRDVSVYKOTQCLICGAPAIGEHNAKGTACKSRPL 180
Db 121 PLNKLDDTEENASAAANAGVNRRCISMDYKOTQCLICGKRPPIGEHNGKSPCTNAY 180
Qy 181 SOGDCPPELKNVTYLEDGDMVDYTGAMDFSTLDTKCEVPLDIOQSTICKYDYIOMSD 240
Db 181 NPGDCPPELINTVYIDQDMVDTFGAMDFTLLQANKSEVPLDICTSICKYDYIKMSE 240
Qy 241 PYGDSMFCLREOLFARHFWNRAGTMDYVPOSLYIKGTGRASPGSCVYSPSGSIV 300
Db 241 PYGDSLFYLRBOHFVRHLFRKACTGVBVDDIYIKGSGSTANLASNFPPTSGSMV 300
Qy 301 TSDQOLFKNPYWLAKRQGHNNICGNQLFVTVVDTTRSTNLTICASTQSPYPGYDATK 360
Db 301 TSDAQIFNKPFWLQRAQGHNNICGNQLFVTVVDTTRSTNLSICAAI-STSETTYKNTN 359
Qy 361 FKQYRHHVEYDLOEITFOLCTITLADVMSYIHSNNSSILEDWNGVPPPTSLVDIYR 420
Db 360 FKEXLRHGEYDLOEITFOLCKITTLADVMTYIHSNNSTILEDWNGLOPPPGTLEDIYR 419
Qy 421 FVQSVAITCOKDAAPAEKNDPDKLFKFWNDLKEKFSLDLQDPYGRKFLVAGLRKRP- 479
Db 420 FVTSQAICQKHPPAPKEDDPLKKTFWENVLKEKFSADLDQPLGRKFLQAGLRKRP 479
Qy 480 -TIG 482
Db 480 FTLG 483
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LOCATION: (0) -- (0)
OTHER INFORMATION: Consensus Sequence
OTHER INFORMATION: At 28 X = K or T
OTHER INFORMATION: At 49 X = Y or F
OTHER INFORMATION: At 53 X = K or R
OTHER INFORMATION: At 54 X = V or A
OTHER INFORMATION: At 119 X = L or F
OTHER INFORMATION: At 131 X = G or S
OTHER INFORMATION: At 132 X = Y or K
OTHER INFORMATION: At 170 X = T or K
OTHER INFORMATION: At 173 X = S or T
OTHER INFORMATION: At 176 X = S or P
OTHER INFORMATION: At 179 X = N or A
OTHER INFORMATION: At 219 X = L or I
OTHER INFORMATION: At 225 X = V or T
OTHER INFORMATION: At 246 X = Y or E
OTHER INFORMATION: At 263 X = T or E
OTHER INFORMATION: At 271 X = D or T
OTHER INFORMATION: At 273 X = L or I
OTHER INFORMATION: At 274 X = V or I
OTHER INFORMATION: At 277 X = G or S
OTHER INFORMATION: At 278 X = N or G
OTHER INFORMATION: At 281 X = S or T
OTHER INFORMATION: At 284 X = A or G
OTHER INFORMATION: At 290 X = H or N
OTHER INFORMATION: At 325 X = H or Q
OTHER INFORMATION: At 346 X = S or T
OTHER INFORMATION: At 347 X = K or T
OTHER INFORMATION: At 348 X = A or S
OTHER INFORMATION: At 366 X = F or Y
OTHER INFORMATION: At 434 X = O or P
OTHER INFORMATION: At 439 X = D or N
OTHER INFORMATION: At 440 X = M or L
OTHER INFORMATION: At 458 X = F or Y
OTHER INFORMATION: At 474 X = T or I
OTHER INFORMATION: At 476 X = A or I
OTHER INFORMATION: At 480 X = I or V
OTHER INFORMATION: At 488 X = P or A
OTHER INFORMATION: At 490 X = T or A
OTHER INFORMATION: At 497 X = T or A
OTHER INFORMATION: At 501 X = K or R
US-08-987-519-3

Query Match      61.4%; Score 1679; DB 2; Length 501;
Best Local Similarity 61.5%; Pred. No. 1.4e-167;
Matches 310; Conservative 69; Mismatches 119; Indels 6; Gaps 4;

QY 3 LMRPNDNTVYLPPPS-VARVNTDDYTRTSIFYHAGSSRLTVGNPFRVPAGGKND 61
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MMRPSDSTVYVPPNPYSKVATDAYKRNIFPHASSRLLVGHPYXSTKX--XNKTV 58
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 62 IPKVSAYQVRFVYVLPDPNKGFLPDSIYNPETQRLVMACAGVEIGRQPLVGSLGHP 121
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 59 VPKVSGYQVRFVYVLPDPNKGFLPDSIYNPETQRLVMACAGVEIGRQPLVGSGHP 118
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 122 FYNKLDDTSSHAATSNVSDVDNVSVDKQPOLCLIGCAPAIGEHMAKGTACKSRPLS 181
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 119 XLNKYDVENSGXGKGPGQDNRNNGMDYKQTLGVGAPLGEHMGKGCXCNXVQ 178
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 182 QGDCPPELEKNTVLEDDMDVDTGAGAMDFTLQDTKCEVPLDQCSICKKPYDLOMSADP 241
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 179 XGDCPPELELTISYVQDDMDVDTGAGAMNFADLOTKNDVXPXIDICGTCKTPIYLOMADP 238
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 242 YGDSMEFCLRRDELFAHFENRAGTMDTVPOSLYIKGTGMRASPGSCVYSPSPSGIVT 301
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 239 YGRLFEFLKKEQMFARHFNFRAGXVGEVPDXLXKXGXNRKSVXSIIYVTPSGSLVS 298
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 302 SDOQLFKRPYMLKKAQGNHNGICMHNOLFVTVYDITSTMLTICASQSPYPGCYDXTKF 361
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 299 SEQOLFEPKPYMLKKAQGNHNGICMHNOLFVTVYDITSTMLTICASQYX--SXYTYSNDY 356
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 362 KQSRHVEEYDLOFIFOLCTITLTADVSTYIHSNNSIILEDQWNGVPPPTTSIYVDYRF 421
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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Db 357 KEYRHVEEXDLOFIFOLCTITLSAEVMAYIHTMNPVSYLEDMWNGLSPPNGTLEDTRY 416
QY 422 VQSVAITCQKDAAPENKDPYDKLFENNVDLKEKFSIDLQDQYPLGRKFLVQAGLR-RKPT 480
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 417 VQSVAITCQKPTPEKEXXDPYKXKXSEFWEVNLKEKESSELDQXPLGRFLLQSGVRGXSKX 476
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 481 IGPRKRSAPSATYSSKPAKRVRR 504
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 477 RTGAKRPVSKXKXAPKRRKXKTK 500
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 14
US-08-724-281-1
; Sequence 1, Application US/08724281
; Patent No. 5874089
; GENERAL INFORMATION:
; APPLICANT: SCHLEGEL, C. Richard
; APPLICANT: JENSON, A. Bennett
; APPLICANT: GHIM, Shih-Je
; TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,281
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,691
; FILING DATE: 02-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teakip, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 010091-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 508 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-724-281-1

Query Match      48.5%; Score 1324.5; DB 2; Length 508;
Best Local Similarity 49.2%; Pred. No. 2.8e-130;
Matches 249; Conservative 88; Mismatches 158; Indels 11; Gaps 8;

QY 1 MALMRPNDNTVYLPPPSVAVVNTDDYTRTSIFYHAGSSRLTVGNPFRVPAGGKND 60
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 7 MAWLPAQNKFEYLPQPIRILSTDEVYTRTNLFYHATSRLLVGHPLEI--SSNQTV 64
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 61 DIPKVSAYQVRFVYVLPDPNKGFLPDSIYNPETQRLVMACAGVEIGRQPLVGSLGSH 120
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 65 TIRKVSNAFRVRRVRADPNRFAFGDKALFNEFETELVWGLGIEIGRQPLGIGTGH 124
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 121 FYNKLDDTSS-SHAATSNVSDVDNVSVDKQPOLCLIGCAPAIGEHMAKGTACKSRP 179
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 125 PLNKLDDDAENPNINVTIANGDSRQNTAFDAKQOTQFLVGCIPASEHNT-SRRCGEG 183
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 180 LSGDCPPELEKNTVLEDDMDVDTGAGAMDFTLQDTKCEVPLDQCSICKKPYDLOMSA 239

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 17, 2003, 10:55:49 ; Search time 28.2831 Seconds
(without alignments)
1723.913 Million cell updates/sec

Title: US-08-913-644-2

Perfect score: 2733
Sequence: 1 MALMRPSDNTVYLPPPSVAR.....APSATTSSKPARVRARRK 507

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR_76:*

1: p1r1:*\n2: p1r2:*\n3: p1r3:*\n4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2719	99.5	568	1 P1WL18	L1 protein - human
2	2450	89.6	539	2 S36566	L1 protein - human
3	2155	78.9	505	1 P1WLPR	L1 protein - human
4	2151	78.7	505	1 P1WL39	L1 protein - human
5	1917.5	70.2	532	2 S36554	L1 protein (altern
6	1909	69.8	531	2 S36537	L1 protein - human
7	1879	68.1	508	2 S36508	L1 protein - human
8	1861.5	68.1	503	2 S36549	L1 protein - human
9	1855	67.9	499	2 S36531	L1 protein - human
10	1851	67.7	534	2 S36583	L1 protein - human
11	1834.5	67.1	504	1 P1WL31	L1 protein - human
12	1820.5	66.6	502	1 S36526	L1 protein - human
13	1804.5	66.0	504	1 P1WL51	L1 protein - human
14	1804.5	66.0	524	1 P1WL58	L1 protein - human
15	1801.5	65.9	529	2 S36578	L1 protein - human
16	1801	65.9	531	1 P1WLHS	major capsid prote
17	1797	65.8	505	1 P1WL35	L1 protein - human
18	1791	65.5	499	1 P1WL33	L1 protein - human
19	1789.5	65.5	510	1 S15620	L1 protein - human
20	1784.5	65.3	510	1 S15627	L1 protein - human
21	1782	65.2	502	1 P1WL1	L1 protein - pygmy
22	1781	65.2	594	2 S36502	L1 protein (altern
23	1771	64.8	505	2 S36589	L1 protein - human
24	1768.5	64.7	500	1 P1WL6	L1 protein - human
25	1766	64.6	505	2 S36560	L1 protein - human
26	1763	64.5	528	2 S36520	L1 protein - human
27	1762	64.5	503	2 S36514	L1 protein - human
28	1759	64.4	499	1 P1WL13	L1 protein - human
29	1757	64.3	502	1 P1WL42	L1 protein - human

30	1733	63.4	501	1 P1WL11	L1 protein - human
31	1724	63.1	502	2 JE0295	L1 protein - human
32	1427	52.2	514	1 P1WL8	L1 protein - human
33	1426.5	52.2	546	2 S36490	L1 protein - human
34	1425.5	52.2	517	2 S36543	L1 protein - human
35	1422.5	52.0	517	2 S36496	L1 protein - human
36	1418	51.9	518	2 S36472	L1 protein - human
37	1416	51.8	507	2 S36595	L1 protein - human
38	1416	51.8	507	2 S36478	L1 protein - human
39	1412.5	51.7	525	1 P1WL85	L1 protein - human
40	1409	51.6	516	1 P1WL5	L1 protein - human
41	1402	51.3	507	2 S36484	L1 protein - human
42	1389	50.8	514	1 P1WL47	L1 protein - human
43	1379.5	50.5	509	2 S36572	L1 protein - human
44	1378.5	50.4	505	1 P1WL8	L1 protein - cotto
45	1338.5	49.0	506	1 P1WL84	L1 protein - bovin

ALIGNMENTS

RESULT 1

L1 protein - human papillomavirus type 18

C:Species: human papillomavirus type 18

C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 24-Feb-1994

C:Accession: A26251

R:Col. S.T.; Danos, O.

A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus typ

A:Reference number: A92937; MID:87283882; PMID:3039146

A:Accession: A26251

A:Molecule type: DNA

A:Residues: 1-568 <COL>

C:Superfamily: papillomavirus L1 protein

C:Keywords: late protein

Query Match 99.5%; Score 2719; DB 1; Length 568;
Best Local Similarity 99.4%; Pred. No. 5.5e-212;
Matches 504; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	MALMRPSDNTVYLPPPSVARVNTDYVTRTSIFYANGSSRLLTVCNPFRRPAGGCKRQ	60
DB	62	MALMRPSDNTVYLPPPSVARVNTDYVTPTSIFYANGSSRLLTVCNPFRRPAGGCKRQ	121
QY	61	DIPKSAIYQRYRFRVQLPDPNKGFLPDSITYNPQRIYACAGVEIGQPLGVLGSH	120
DB	122	DIPKSAIYQRYRFRVQLPDPNKGFLPDSITYNPQRIYACAGVEIGQPLGVLGSH	181
QY	121	PFYNNKLDTESSHAATSNVSEEDVNDVYKOTOLCIIGCAPAIGEHNAKGTACKSRPL	180
DB	182	PFYNNKLDTESSHAATSNVSEEDVNDVYKOTOLCIIGCAPAIGEHNAKGTACKSRPL	241
QY	181	SGQDCPEPLEKNTVLEDDGMVDTGYGAMDESTLQDTKCEVPLDICSICKPYDIOMSD	240
DB	242	SGQDCPEPLEKNTVLEDDGMVDTGYGAMDESTLQDTKCEVPLDICSICKPYDIOMSD	301
QY	241	PYDSMFPCRLRRQLFARHFWNAGTMDGPVPSLTIKYGGMASGSCVYSPSGSTY	300
DB	302	PYDSMFPCRLRRQLFARHFWNAGTMDGPVPSLTIKYGGMASGSCVYSPSGSTY	361
QY	301	TSDSQLEFNKRYWLHKAQGHNGICWNQLEFVTVDTTRSTNLITICASTOSPVGQYDATR	360
DB	362	TSDSQLEFNKRYWLHKAQGHNGICWNQLEFVTVDTTRSTNLITICASTOSPVGQYDATR	421
QY	361	FKYISRAVEYDQIFQOLCTITLTADVMSYHSNASSILEDNFGVPPPTSLVDYTR	420
DB	422	FKYISRAVEYDQIFQOLCTITLTADVMSYHSNASSILEDNFGVPPPTSLVDYTR	481
QY	421	FVQSVATTCOKDAAPENKDPYDKLFWMVNDLKEKSLIDQYPLGRKFLYQAGLRKRP	480
DB	482	FVQSVATTCOKDAAPENKDPYDKLFWMVNDLKEKSLIDQYPLGRKFLYQAGLRKRP	541

QY 481 IGPKRKRSAPATSSSKPAKRVVRARK 507
 Db 542 IGPKRKRSAPATSSSKPAKRVVRARK 568

RESULT 2

S36566

L1 protein - human papillomavirus type 45

C:Species: human papillomavirus type 45

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S36566; F44889

R:Deilus, H.; Hofmann, B.

Submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36566

A:Molecule type: DNA

A:Residues: 1-539

R:van den Brule, A.J.; Snijders, P.J.; Raaphorst, P.M.; Schrijnemakers, H.F.; Deilus, H.

J. Clin. Microbiol. 30, 1716-1721, 1992

A:Title: General primer polymerase chain reaction in combination with sequence analysis

A:Reference number: A44889; MUID:92332706; PMID:1321168

A:Accession: F44889

A:Molecule type: DNA

A:Residues: 366-399 <YAN>

A:Cross-references: GB:S40261; NID:9251692; PIDN:AA82567.1; PID:9251693

A:Experimental source: mucosotropic type 45, cervical smear

A:Note: sequence extracted from NCBI backbone (NCBIN:109396, NCBI:P:109413)

C:Superfamily: Papillomavirus L1 protein

C:Keywords: late protein

Query Match 89.6%, Score 2450; DB 2; Length 539;
 Best Local Similarity 87.3%, Pred. No. 3e-190;
 Matches .448; Conservative 30; Mismatches 29; Indels 6; Gaps 3;

QY 1 MALRPSDNVYLLPPPSAVRVNDDYVTRTSIFYHAGSSRLTVGNPYFR-VAGAGGNK 59
 Db 27 MALRPSDNVYLLPPPSAVRVNDDYVTRTSIFYHAGSSRLTVGNPYFRVPPNGAGNK 86
 QY 60 QDIPVSAVOYRVFVQLPDPNKFGLPDSIYNPETOFLVMACAVEIGRGQPLVGLSG 119
 Db 87 QAVPKVSAVOYRVFVQLPDPNKFGLPDSIYNPETOFLVMACAVEIGRGQPLVGLSG 146
 QY 120 HPEFNKLDLDTSSHAATSNVSEVDYRDVNSVDYKOTQCLICGAPAIGEHMAKGTACKSRP 179
 Db 147 HPEFNKLDLDTSSHAATAAATAVITQDVRDVSVDYKOTQCLICGAPAIGEHMAKGTACKSRP 206
 QY 180 LSGDCCPLELKNVLEEDGMDVDTGYGAMDESLDTDFCEVPLDTCOSICKYPPYLQMSA 239
 Db 207 LQPDCCPLELKNVLEEDGMDVDTGYGAMDESLDTDFCEVPLDTCOSICKYPPYLQMSA 266
 QY 240 DPGDSMEFCLRRQLFAHFHFNWAGTMDVPSLYIKGT--GMRASPGSCVSPSPSG 297
 Db 267 DPGDSMEFCLRRQLFAHFHFNWAGTMDVPSLYIKGT--GMRASPGSCVSPSPSG 326
 QY 298 STVSDSGLFKPFWLKAQCHNNGICWNOLEFVYVDTTRSTNLTICASTQSPVPGQYD 357
 Db 327 STVSDSGLFKPFWLKAQCHNNGICWNOLEFVYVDTTRSTNLTICASTQSPVPGQYD 386
 QY 358 ATKFOYSRHYEEDLQFIOLCTITLADVMSTIHSNNSIILDMNCGVPPPTSLYD 417
 Db 387 PTKFOYSRHYEEDLQFIOLCTITLADVMSTIHSNNSIILDMNCGVPPPTSLYD 446
 QY 418 TYRFVQSAVATCQKDAAPAEKNDPYDKLKFNNVDLKEKFSIDLQYPLGRKFLVQAGLR 477
 Db 447 TYRFVQSAVATCQKDAAPAEKNDPYDKLKFNNVDLKEKFSIDLQYPLGRKFLVQAGLR 506
 QY 478 KPTIGPKRRSAP---ATTSSKPAKRVVRARK 507
 Db 507 RPTIGPKRRSAPASTSTASTASRPAKRVVRARK 539

RESULT 3

P1M18R

L1 protein - human papillomavirus type ME180 (provirus)

C:Species: human papillomavirus type ME180

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 28-Jul-2000

C:Accession: B40509

R:Reuter, S.; Deilus, H.; Kohn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.

J. Virol. 65, 5564-5568, 1991

A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma

A:Reference number: A40509; MUID:91374616; PMID:1716694

A:Accession: B40509

A:Status: translation not shown

A:Molecule type: DNA

A:Cross-references: GB:M73258; NID:9184383; PIDN:AAFI4010.1; PID:96478870

A:Superfamily: Papillomavirus L1 protein

C:Keywords: late protein

Query Match 76.9%, Score 2155; DB 1; Length 505;
 Best Local Similarity 76.7%, Pred. No. 2.1e-166;
 Matches 386; Conservative 52; Mismatches 65; Indels 0; Gaps 0;

QY 1 MALRPSDNVYLLPPPSAVRVNDDYVTRTSIFYHAGSSRLTVGNPYFRVPPNGAGNK 60
 Db 1 MALRPSDNVYLLPPPSAVRVNDDYVTRTSIFYHAGSSRLTVGNPYFRVPPNGAGNK 60
 QY 61 DIPVSAVOYRVFVQLPDPNKFGLPDSIYNPETOFLVMACAVEIGRGQPLVGLSG 120
 Db 61 DIPVSAVOYRVFVQLPDPNKFGLPDSIYNPETOFLVMACAVEIGRGQPLVGLSG 120
 QY 121 PFKNKLDLDTSSHAATSNVSEVDYRDVNSVDYKOTQCLICGAPAIGEHMAKGTACKSRP 180
 Db 121 PFKNKLDLDTSSHAATSNVSEVDYRDVNSVDYKOTQCLICGAPAIGEHMAKGTACKSRP 180
 QY 181 SQGDCPPELKNVLEEDGMDVDTGYGAMDESLDTDFCEVPLDTCOSICKYPPYLQMSAD 240
 Db 181 SQGDCPPELKNVLEEDGMDVDTGYGAMDESLDTDFCEVPLDTCOSICKYPPYLQMSAD 240
 QY 241 PYGDSMEFCLRRQLFAHFHFNWAGTMDVPSLYIKGTGMRASPGSCVSPSPSG 300
 Db 241 PYGDSMEFCLRRQLFAHFHFNWAGTMDVPSLYIKGTGMRASPGSCVSPSPSG 300
 QY 301 TSQSOLFKPFWLKAQCHNNGICWNOLEFVYVDTTRSTNLTICASTQSPVPGQYD 360
 Db 301 TSQSOLFKPFWLKAQCHNNGICWNOLEFVYVDTTRSTNLTICASTQSPVPGQYD 360
 QY 361 FKQYSRHYEEDLQFIOLCTITLADVMSTIHSNNSIILDMNCGVPPPTSLYD 420
 Db 361 FKQYSRHYEEDLQFIOLCTITLADVMSTIHSNNSIILDMNCGVPPPTSLYD 420
 QY 421 FVQSAVATCQKDAAPAEKNDPYDKLKFNNVDLKEKFSIDLQYPLGRKFLVQAGLR 480
 Db 421 FVQSAVATCQKDAAPAEKNDPYDKLKFNNVDLKEKFSIDLQYPLGRKFLVQAGLR 480
 QY 481 IGPKRKRSAPATSSSKPAKRVVRARK 503
 Db 481 IGPKRKRSAPATSSSKPAKRVVRARK 503

RESULT 4

P1M139

L1 protein - human papillomavirus type 39

C:Species: human papillomavirus type 39

A:Note: host Homo sapiens (man)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999

C:Accession: H38502

R:Voipiers, C.; Strebeck, R.E.

Virology 181, 419-423, 1991

A:Title: Genome organization and nucleotide sequence of human papillomavirus type 39.

A:Reference number: A38502; MUID:91135017; PMID:1847266

A:Accession: H38502

A:Status: translation not shown

A:Molecule type: DNA
 A:Residues: 1-505 <VOL>
 A:Cross-references: GB:M62849; EMBL:M38185; NID:g333245; PIDN:AAA47056.1; PID:g463192
 C:Superfamily: papillomavirus L1 protein
 C:Keywords: late protein

Query Match 78.7%; Score 2151; DB 1; Length 505;
 Best Local Similarity 77.3%; Pred. No. 4.3e-166;

Matches 391; Conservative 48; Mismatches 61; Indels 6; Gaps 3;

```

QY 1 MALMRSDNTVYLPPPSVAVVNTDDYVTRTSIFTHAGSSRLITVGNPFRVAGAGNKO 60
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MALMRSDNTVYLPPPSVAVVNTDDYVTRTSIFTHAGSSRLITVGNPFRVAGAGNKO 60
QY 61 DIPKVSAYQYRVFRVQLPDNKFGLPDNSIYNPETORLWACAGVEIGRGQPLGVLSGH 120
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 DIPKVSAYQYRVFRVQLPDNKFGLPDNSIYNPETORLWACAGVEIGRGQPLGVLSGH 120
QY 121 PFYKRLDDTRESSHAATSNVSEYRDVNSVDYKOTQCTICGAPAIQEHNAKGTACKSRPL 180
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 PFYKRLDDTRESSHAATSNVSEYRDVNSVDYKOTQCTICGAPAIQEHNAKGTACKSRPL 179
QY 181 SOGDCEPLELKNVLEEDGDMVDVDTGYGAMPSTLQDTRKEVPLDTCOSICKYPPYLQMSAD 240
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 180 SOGDCEPLELKNVLEEDGDMVDVDTGYGAMPSTLQDTRKEVPLDTCOSICKYPPYLQMSAD 239
QY 241 PYGDSMFCLRRQQLFARHFWNAGTMDTVPQSLYIKGTGMRASPGSCVYSPSPGSIV 300
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 240 PYGDSMFCLRRQQLFARHFWNAGTMDTVPQSLYIKGTGMRASPGSCVYSPSPGSIV 299
QY 301 TSPSOLFNRPYWLRHKAQGHNGICMHNQLFVYVDTTRSTNLTICASTGSPVPGQIDAK 360
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 300 TSPSOLFNRPYWLRHKAQGHNGICMHNQLFVYVDTTRSTNLTICASTGSPVPGQIDAK 359
QY 361 FKQYSHREYEDLQFIQCTITLFDVMSYIHSNMSILEDNFGVPPPTSLVDYTR 420
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 360 FKQYSHREYEDLQFIQCTITLFDVMSYIHSNMSILEDNFGVPPPTSLVDYTR 419
QY 421 FVQSVATTCOKDAAPAEKNDPYDKLFKFWNDLKEKESLDDQYPLGKFLVQAGLRKPT 480
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 420 YLQSAITCOKDAAPAEKNDPYDKLFKFWNDLKEKESLDDQYPLGKFLVQAGLRKPT 479
QY 481 IGPRKRSAPSATSSKPA---KRVV 503
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 480 IGPRKR--PAASTSSSATKKKKRV 503

```

RESULT 5 S36554

L1 protein (alternative) - human papillomavirus type 3

C:Species: human papillomavirus type 3
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S36554

R:Delius, H.; Hofmann, B.
 Submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36554

A:Molecule type: DNA

A:Residues: 1-532

A:Cross-references: EMBL:X74462; NID:g397005; PIDN:CAA52474.1; PID:g397012

C:Superfamily: papillomavirus L1 protein

C:Keywords: late protein

Query Match 70.2%; Score 1917.5; DB 2; Length 532;
 Best Local Similarity 68.8%; Pred. No. 3.7e-147;
 Matches 351; Conservative 65; Mismatches 85; Indels 9; Gaps 4;

```

Db 89 DIPKVSAYQYRVFRVRLPDNKFGLPDARLYNDASRLWACAGVEIGRGQPLGVLSGH 148
QY 121 PFYKRLDDTRESSHAATSNVSEYRDVNSVDYKOTQCTICGAPAIQEHNAKGTACKSRPL 180
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 149 PFYKRLDDTRESSHAATSNVSEYRDVNSVDYKOTQCTICGAPAIQEHNAKGTACKSRPL 180
QY 181 SOGDCEPLELKNVLEEDGDMVDVDTGYGAMPSTLQDTRKEVPLDTCOSICKYPPYLQMSAD 240
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 208 SPGDCEPLELITAPIDQGDMDVDVDTGYGAMPSTLQDTRKEVPLDTCOSICKYPPYLQMSAD 267
QY 241 PYGDSMFCLRRQQLFARHFWNAGTMDTVPQSLYIKGTGMRASPGSCVYSPSPGSIV 300
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 268 PYGDSMFCLRRQQLFARHFWNAGTMDTVPQSLYIKGTGMRASPGSCVYSPSPGSIV 300
QY 298 SIYTSOQLFNRPYWLRHKAQGHNGICMHNQLFVYVDTTRSTNLTICASTGSPVPGQIDAK 357
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 328 SMVTSEOLFNRPYWLRHKAQGHNGICMHNQLFVYVDTTRSTNLTICASTGSPVPGQIDAK 385
QY 358 ATKFKQYSHREYEDLQFIQCTITLFDVMSYIHSNMSILEDNFGVPPPTSLVDYTR 417
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 386 ATKFKQYSHREYEDLQFIQCTITLFDVMSYIHSNMSILEDNFGVPPPTSLVDYTR 445
QY 418 TYPVQSVATTCOKDAAPAEKNDPYDKLFKFWNDLKEKESLDDQYPLGKFLVQAGLRK 477
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 446 TYPVQSVATTCOKDAAPAEKNDPYDKLFKFWNDLKEKESLDDQYPLGKFLVQAGLRK 505
QY 478 KPTIGPRKRSAPSATSSKPAKRVVRAK 507
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 506 KRSISVAKR--SATTTSTAAAKRKRTK 532

```

RESULT 6 S36537

L1 protein - human papillomavirus type 10

C:Species: human papillomavirus type 10
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S36537

R:Delius, H.; Hofmann, B.
 Submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36537

A:Molecule type: DNA

A:Residues: 1-531

A:Cross-references: EMBL:X74465; NID:g396901; PIDN:CAA52494.1; PID:g396908

C:Superfamily: papillomavirus L1 protein

C:Keywords: late protein

Query Match 69.8%; Score 1909; DB 2; Length 531;
 Best Local Similarity 67.9%; Pred. No. 1.8e-146;
 Matches 342; Conservative 70; Mismatches 90; Indels 2; Gaps 2;

```

QY 1 MALMRSDNTVYLPPPSVAVVNTDDYVTRTSIFTHAGSSRLITVGNPFRVAGAGNKO 60
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 29 MALMRSDNTVYLPPPSVAVVNTDDYVTRTSIFTHAGSSRLITVGNPFRVAGAGNKO 88
QY 61 DIPKVSAYQYRVFRVQLPDNKFGLPDNSIYNPETORLWACAGVEIGRGQPLGVLSGH 120
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 89 DIPKVSAYQYRVFRVRLPDNKFGLPDARLYNDASRLWACAGVEIGRGQPLGVLSGH 148
QY 121 PFYKRLDDTRESSHAATSNVSEYRDVNSVDYKOTQCTICGAPAIQEHNAKGTACKSRPL 180
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 149 PFYKRLDDTRESSHAATSNVSEYRDVNSVDYKOTQCTICGAPAIQEHNAKGTACKSRPL 180
QY 181 SOGDCEPLELKNVLEEDGDMVDVDTGYGAMPSTLQDTRKEVPLDTCOSICKYPPYLQMSAD 240
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 208 SPGDCEPLELITAPIDQGDMDVDVDTGYGAMPSTLQDTRKEVPLDTCOSICKYPPYLQMSAD 267
QY 241 PYGDSMFCLRRQQLFARHFWNAGTMDTVPQSLYIKGTGMRASPGSCVYSPSPGSIV 300
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 268 PYGDSMFCLRRQQLFARHFWNAGTMDTVPQSLYIKGTGMRASPGSCVYSPSPGSIV 327

```

```
OY 301 TSDQLFKNPKYWLAKAGCHNNGICMHNQLEFVTVVDTTRSTNLITICASTQSPGQYDATK 360
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 328 TSEQLFKNPKYWLAKAGCHNNGICMHNQLEFVTVVDTTRSTNLITICASTQSPGQYDATK 387
OY 361 FKQSRHVEEYDLOFIFOLCTITLADVMYSIHSMNSIILEDNNGVPPPTSLVDYR 420
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 388 FKEILRHGEYDLOFIFOLCTITLADVMYSIHSMNSIILEDNNGVPPPTSLVDYR 447
OY 421 FVQSVATCQKDAAPAEKNDPYDKLFKNVNDLKEKFSIDLDOYPLGRKFLVQAGLRKPT 480
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 448 FLSSAATCQKDPTEKQDYAKLNFWDVDLKDQFSLDQFPLGRKFLVQAGLRKPT 507
OY 481 IGRKRSAPSATSSKPAKRRVR 504
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 508 VSVKRRAPATSA-TGSTAKRRRTK 530
```

RESULT 7

```
S36508
L1 protein - human papillomavirus type 30
C:Species: human papillomavirus type 30
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S36508
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36508
A:Molecule type: DNA
A:Residues: 1-508 <DEL>
A:Cross-references: EMBL:X74474; NID:q396973; PIDN:CAA52548.1; PID:q396980
C:Superfamily: papillomavirus L1 protein
C:Keywords: late protein
```

```
Query Match 68.8%; Score 1879; DB 2; Length 508;
Best Local Similarity 67.1%; Pred. No. 4.5e-144;
Matches 337; Conservative 82; Mismatches 81; Indels 2; Gaps 1;
```

```
OY 1 MALRPSDNITYLPPPSARVYVNDYVTRTSIFTHAGSSRLTVGNPFYRVPAAGGNKQ 60
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 8 MAVNPSSTKYLLPPTPVSKYVPTDAYKRNIFVHAGSSRLTVGNPFYRVPAAGGNKQ 67
OY 61 DIPKSAVQYVRFVQLPDPNKFGLPDNSIYNPETORLVWACAGVEIGRQPLGVLGSGH 120
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 68 DIPKSAVQYVRFVQLPDPNKFGLPDNSIYNPETORLVWACAGVEIGRQPLGVLGSGH 127
OY 121 PFYKRLDTESSHAATSVSEVDVNDYKQFQCLIGCAPAIGEMAKGTACKSRPL 180
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 128 PLFNKLDTESSHAATSVSEVDVNDYKQFQCLIGCAPAIGEMAKGTACKSRPL 187
OY 181 SOGCPPELEKNTYLEGDMDVDTGFGAMDPESTLDTCFCEVPLDTCOSICKYPTDIQMSAD 240
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 188 AOGDCEPLELSTIIEBDMIDTGFQAMDFTALDTSVPTDLSQSTCKPDLTKMSAD 247
OY 241 PYGDSMFECFLRREOLFARHFNNRAGTMDVTPQSLYIKGTGMRASPGSCVSPSPSGSI 300
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 248 AYGSMSWYLRREOLFARHFNNRAGTMDVTPQSLYIKGTGMRASPGSCVSPSPSGSI 307
OY 301 TSDSOLFKNPKYWLAKAGCHNNGICMHNQLEFVTVVDTTRSTNLITICASTQSPGQYDATK 360
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 308 TSEQLFKNPKYWLAKAGCHNNGICMHNQLEFVTVVDTTRSTNLITICASTQSPGQYDATK 365
OY 361 FKQSRHVEEYDLOFIFOLCTITLADVMYSIHSMNSIILEDNNGVPPPTSLVDYR 420
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 366 IKQYVRHVEEYDLOFIFOLCTITLADVMYSIHSMNSIILEDNNGVPPPTSLVDYR 425
OY 421 FVQSVATCQKDAAPAEKNDPYDKLFKNVNDLKEKFSIDLDOYPLGRKFLVQAGLRKPT 480
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 426 YKSLATTCQKQDQPAEKEDPLAKTFKFDVNDLQDSFADLQFPLGRKFLVQAGLRKPT 485
OY 481 IGRKRSAPSATSSKPAKRRVR 502
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 486 TTTKRSAPSSSTSTSPSAKRRR 507
```

RESULT 8

S36549

```
L1 protein - human papillomavirus type 26
C:Species: human papillomavirus type 26
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S36549
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36549
A:Molecule type: DNA
A:Residues: 1-503 <DEL>
A:Cross-references: EMBL:X74472; NID:q396956; PIDN:CAA52535.1; PID:q396963
C:Superfamily: papillomavirus L1 protein
C:Keywords: late protein
```

```
Query Match 68.1%; Score 1861.5; DB 2; Length 503;
Best Local Similarity 67.3%; Pred. No. 1.2e-142;
Matches 337; Conservative 70; Mismatches 91; Indels 3; Gaps 3;
```

```
OY 1 MALRPSDNITYLPPPSARVYVNDYVTRTSIFTHAGSSRLTVGNPFYRVPAAGGNKQ 60
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MALRPSDNITYLPPPSARVYVNDYVTRTSIFTHAGSSRLTVGNPFYRVPAAGGNKQ 60
OY 61 DIPKSAVQYVRFVQLPDPNKFGLPDNSIYNPETORLVWACAGVEIGRQPLGVLGSGH 120
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 DIPKSAVQYVRFVQLPDPNKFGLPDNSIYNPETORLVWACAGVEIGRQPLGVLGSGH 119
OY 121 PFYKRLDTESSHAATSVSEVDVNDYKQFQCLIGCAPAIGEMAKGTACKSRPL 180
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 PLFNKLDTESSHAATSVSEVDVNDYKQFQCLIGCAPAIGEMAKGTACKSRPL 179
OY 181 SOGCPPELEKNTYLEGDMDVDTGFGAMDPESTLDTCFCEVPLDTCOSICKYPTDIQMSAD 240
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 QRGDCEPLELSTIIEBDMIDTGFQAMDFTALDTSVPTDLSQSTCKPDLTKMSAD 239
OY 241 PYGDSMFECFLRREOLFARHFNNRAGTMDVTPQSLYIKGT-GMRASPGSCVSPSPSGSI 299
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 TYGNSMFEFLRREOLFARHFNNRAGTMDVTPQSLYIKGT-GMRASPGSCVSPSPSGSI 299
OY 300 VTSOQLFKNPKYWLAKAGCHNNGICMHNQLEFVTVVDTTRSTNLITICASTQSPGQYDAT 359
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 VTSOQLFKNPKYWLAKAGCHNNGICMHNQLEFVTVVDTTRSTNLITICASTQSPGQYDAT 359
OY 360 FKQSRHVEEYDLOFIFOLCTITLADVMYSIHSMNSIILEDNNGVPPPTSLVDYR 419
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 360 DYKQFIRHGEYDLOFIFOLCTITLADVMYSIHSMNSIILEDNNGVPPPTSLVDYR 419
OY 420 FVQSVATCQKDAAPAEKNDPYDKLFKNVNDLKEKFSIDLDOYPLGRKFLVQAGLRKPT 479
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 420 RFIKNSATTCQKQDQPAEKEDPLAKTFKFDVNDLQDSFADLQFPLGRKFLVQAGLRKPT 479
OY 480 TIGRKSAPSATSSKPAKRRVR 500
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 480 KLG-TKRLPSTSSSTRKRRR 499
```

RESULT 9

S36531

```
L1 protein - human papillomavirus type 53
C:Species: human papillomavirus type 53
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S36531
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36531
A:Molecule type: DNA
A:Residues: 1-499 <DEL>
```

A:Cross-references: EMBL:X74482; NID:q397046; PIDN:CA45295.1; PID:q397052
C:Superfamily: Papillomavirus L1 protein
C:Keywords: late protein

Query Match 67.9%; Score 1855; DB 2; Length 499;
Best Local Similarity 66.3%; Pred. No. 3.9e-142;
Matches 333; Conservative 78; Mismatches 87; Indels 4; Gaps 2;

```
OY 1 MALMRPSNTVYLLPPPSVAVVNTDDYVTRTSIFYHAGSSRLITVGNPFYRVPAGGKQ 60
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MAWMPSSDSKYLLPPTPVSKVITTDAYKRTIFYHAGSSRLITVGHPPYISKSG--KA 58
61 DIPKSAQYQYRFRVRLPDPNKFGLPDNSIYNPETQRLVMACAGYEIGRQPLGVLGSH 120
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 59 DIPKSAQYQYRFRVRLPDPNKFGLPDNINPDERLVMACVGLIEGRQPLGVLGSH 118
121 PFYKRLDTESSHAATSNVSEVDYRDNVSVYKQIOLCLICAPALGEHMAKGTACKSRPL 180
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 119 PLFNRLDTESSHAATSNVSEVDYRDNVSVYKQIOLCLICAPALGEHMAKGTACKSRPT 178
OY 181 SOGDCPPELEKNTVLEDGDMVDYTGAMDFSTLDQKCEVPLDIOCSICKYDYLOMSAD 240
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 179 TAGDCPPELEKNTVLEDGDMVDYTGAMDFSTLDQKCEVPLDIOCSICKYDYLOMSAD 238
OY 241 PYGDSMEFCLRRQDLFAHFHNNRAGTMGDTVPQSLYIKGTGRASPGSCVSPSPSGITV 300
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 239 AYGDSMWFYLRREQLFTHFFRAGVIGETIPNDIYIGSNGRDPSPSYATPSGSMI 298
OY 301 TSDSOLFKNPYWLAHQGNHNCICWNOLEFVTVVDTTRSTNLTICASTQSPVPGQYDATK 360
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 299 TSEAOLEFKNPYWLAHQGNHNCICWNOLEFVTVVDTTRSTNLTICASTQSPVPGQYDATK 356
OY 361 FKQYRHAEEYLOLFQOLCTITLADVMSYHNSNLSLEDMNFGVPPPTSLVDYTR 420
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 357 IKQYRHAEEYLOLFQOLCTITLADVMSYHNSNLSLEDMNFGVPPPTSLVDYTR 416
OY 421 FVQSAITCQKDAAPAEKNDPYDKLFMNVDLKEKFSLDLOYPLGRKFLVAGLRKPT 480
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 417 YKSAITCQKDAAPAEKNDPYDKLFMNVDLKEKFSLDLOYPLGRKFLVAGLRKPT 476
OY 481 IGPRKRSAPSATSTSSKPAKRVR 502
  :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 477 VSSKRSASTSTSSKPAKRVR 498
```

RESULT 10

L1 protein - human papillomavirus type 56
S36583
C:Species: human papillomavirus type 56
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S36583; H4489
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36583
A:Molecule type: DNA
A:Residues: 1-534
A:Cross-references: EMBL:X74483; NID:q397053; PIDN:CA452600.1; PID:q397059
R:van den Brule, A.J.; Snijders, P.J.; Raaphorst, P.M.; Schrijnemakers, H.F.; Delius, H.
J. Clin. Microbiol. 30, 1716-1721, 1992
A:Title: General primer polymerase chain reaction in combination with sequence analysis
A:Reference number: A44899; MID:92332706; PMID:1321168
A:Accession: H44899
A:Molecule type: DNA
A:Residues: 371-402 <VAN>
A:Cross-references: NID:q251696; PIDN:AA822569.1; PID:q251697
A:Experimental source: mucosotropic type 56, cervical smear
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:109398, NCBIP:109406)
C:Superfamily: papillomavirus L1 protein
C:Keywords: late protein

Query Match 67.7%; Score 1851; DB 2; Length 534;
Best Local Similarity 67.0%; Pred. No. 9e-142;
Matches 337; Conservative 71; Mismatches 89; Indels 6; Gaps 4;

```
OY 1 MALMRPSNTVYLLPPPSVAVVNTDDYVTRTSIFYHAGSSRLITVGNPFYRVPAGGKQ 60
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 36 MATWMPSEKVTYLLPPTPVSKVATDSYKRTISIFYHAGSSRLAVGHPYISY--TYDNKTY 94
61 DIPKSAQYQYRFRVRLPDPNKFGLPDNSIYNPETQRLVMACAGYEIGRQPLGVLGSH 120
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 95 NIPKSAQYQYRFRVRLPDPNKFGLPDNINPDERLVMACVGLIEGRQPLGVLGSH 154
121 PFYKRLDTESSHAATSNVSEVDYRDNVSVYKQIOLCLICAPALGEHMAKGTACKSRPL 180
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 155 PLFNRLDTESSHAATSNVSEVDYRDNVSVYKQIOLCLICAPALGEHMAKGTACKSRPT 214
OY 181 SOGDCPPELEKNTVLEDGDMVDYTGAMDFSTLDQKCEVPLDIOCSICKYDYLOMSAD 240
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 215 TTGDCPPELEKNTVLEDGDMVDYTGAMDFSTLDQKCEVPLDIOCSICKYDYLOMSAD 274
OY 241 PYGDSMEFCLRRQDLFAHFHNNRAGTMGDTVPQSLYIKGTGRASPGSCVSPSPSGITV 300
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 275 AYGDSMWFYLRREQLFTHFFRAGVIGETIPAEILYLGSGNREPPSPSYATPSGSMI 334
OY 301 TSDSOLFKNPYWLAHQGNHNCICWNOLEFVTVVDTTRSTNLTICASTQSPVPGQYDATK 360
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 335 TSEAOLEFKNPYWLAHQGNHNCICWNOLEFVTVVDTTRSTNLTICASTQSPVPGQYDATK 392
OY 361 FKQYRHAEEYLOLFQOLCTITLADVMSYHNSNLSLEDMNFGVPPPTSLVDYTR 420
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 393 IKQYRHAEEYLOLFQOLCTITLADVMSYHNSNLSLEDMNFGVPPPTSLVDYTR 452
OY 421 FVQSAITCQKDAAPAEKNDPYDKLFMNVDLKEKFSLDLOYPLGRKFLVAGLRKPT 480
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 453 YKSAITCQKDAAPAEKNDPYDKLFMNVDLKEKFSLDLOYPLGRKFLVAGLRKPT 512
OY 481 IGPRKRSAPSATSTSSKPAKRVR 502
  :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 513 VSSKRSASTSTSSKPAKRVR 498
```

RESULT 11

L1 protein - human papillomavirus type 31
PIWL31
C:Species: human papillomavirus type 31
A:Note: host Homo sapiens (man)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
R:Goldsbrough, M.D.; Dislvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-as
A:Reference number: A94398; MID:89299478; PMID:2545036
A:Accession: G32444
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-504 <GOL>
A:Cross-references: GB:J04353; NID:q333048; PIDN:AAA46956.1; PID:q459922
C:Superfamily: papillomavirus L1 protein
C:Keywords: late protein

Query Match 67.1%; Score 1834.5; DB 1; Length 504;
Best Local Similarity 65.1%; Pred. No. 1.8e-140;
Matches 329; Conservative 79; Mismatches 94; Indels 3; Gaps 3;

```
OY 1 MALMRPSNTVYLLPPPSVAVVNTDDYVTRTSIFYHAGSSRLITVGNPFYRVPAGGKQ 60
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MSLMRPSKATYLLPPTPVSKVATDSYKRTISIFYHAGSSRLAVGHPYISY--TYDNKTY 60
OY 61 -DIPKSAQYQYRFRVRLPDPNKFGLPDNSIYNPETQRLVMACAGYEIGRQPLGVLGSH 119
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 IYVPKVSQYQYRFRVRLPDPNKFGLPDNINPDERLVMACVGLIEGRQPLGVLGSH 120
OY 120 HFFYKRLDTESSHAATSNVSEVDYRDNVSVYKQIOLCLICAPALGEHMAKGTACKSRP 179
```

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Db      121 HPLNFKEDTENNRRYAGPPTDNRCISMDYKOTQLCLGCKPPIGEHMGKSPCSNNA 180
      180 LSGDPPPLELKTNYLEDGMVDTGYGAMDFSTLDQTKCEVPDLCOSICKYDYLOMSA 239
      181 ITTGDDPPLEKNSVLDGDMVDYFGAMDFTALDQTKSNVPLDICSICKYDYLOMSA 240
      240 DPYGDSPFCLRRQDLFARHFNWAGTMDGTPOSILYKGTGKARASPGSCVSPSPSGT 299
      241 EPGYDGLTFEFLRQEGVFHFRFNRSGTGESVPTDLYIKSGSTALANSTYPTPSGSM 300
      300 VTSDSOLFENKPYLHRAQGNNGICWNOLFTVYVDTTRSTNLTICASTOSPPVPGQYAT 359
      301 VTSDAOIFENKPYMORAGNNGICWNOLFVTVVDTTRSTNMSVCAAIANS-DTTFKSS 359
      360 KFKOYSHVEYDLOLTFOLCTTLTADVMSYIHSNNSLTEDMNGVPPPTSLVDY 419
      360 NFKYLRHGEEDLOLTFOLCTTLTADVMSYIHSNMPALTEDMNGVPPPTSLVDY 419
      420 RPYOAVITCQKDAAPENKDPYDKLTFMNVDLKEKFSLDLDQYPLGKRFVLQAGLRKP 479
      420 RPYTSQAITCQKTAPOKPKEDPKDYFVFNKKEKFSADLDQPLGKRFVLQAGLRAR 479
      480 TIGPKRSAPSATSSKPAKRVYR 504
      480 KFKARNSAPASSTTT-PAKRRKTK 503

```

RESULT 12

```

S36526
LI protein - human papillomavirus type 35H
C:Species: human papillomavirus type 35H
C>Date: 09-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999
C:Accession: S36526
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36526
A:Molecule type: DNA
A:Residues: 1-502 <DEL>
A:Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52566.1; PID:g397004
A:Experimental source: strain 35H
C:Superfamily: papillomavirus LI protein
C:Keywords: late protein

```

```

Query Match      66.6%; Score 1820.5; DB 2; Length 502;
Best Local Similarity 65.1%; Pred. No. 2.4e-139;
Matches 329; Conservative 70; Mismatches 103; Indels 3; Gaps 2;

      1 MALWRPSDNTVYLPSPSVARVNTDVTYRTSIFHYAGSSRLTLVGNPFRVPAGGKNQ 60
      1 MSLMRSSEATVYLPSPSVKVSSTDEVYRTNITYHAGSSRLAVGHYAIKKNODNKI 60
      61 DIRKVSAYQYRVRRVQLDPDNKFGLPDINSIYNPETORLVACAGVEIGRQPLGVLGSH 120
      61 AVKRVSGIQYRVRRVQLDPDNKFGEPDTSFYDPAQRLLVACAGVEIGRQPLGVLGSH 120
      121 PFYNNKLDDESSHAATSNVEDYRVNVDYKOTQLCTICAPALGHNKGTACKSRPL 180
      121 PLANKLDDTENSNNKYVNGSSTDNRECLSMYKOTQLCTICAPALGHNKGTACKSRPL 180
      181 SGGDPPPLELKTNYLEDGMVDTGYGAMDFSTLDQTKCEVPDLCOSICKYDYLOMSAD 240
      181 KAGSCPPLELKTNYLEDGMVDTGYGAMDFSTLDQTKCEVPDLCOSICKYDYLOMSAD 240
      241 PYGDSMFFCLRRQDLFARHFNWAGTMDGTPOSILYKGTGKARASPGSCVSPSPSGT 300
      241 PYGDMFFCLRRQDLFARHFNWAGTMDGTPOSILYKGTGKARASPGSCVSPSPSGT 300
      301 TSDSOLFENKPYLHRAQGNNGICWNOLFTVYVDTTRSTNLTICASTOSPPVPGQYAT 360
      299 TSDQOLFENKPYLHRAQGNNGICWNOLFVTVVDTTRSTNMSVCAVSSS-DSTYKNDN 357

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      361 KFKOYSHVEYDLOLTFOLCTTLTADVMSYIHSNNSLTEDMNGVPPPTSLVDY 420
      358 KFKYLRHGEEDLOLTFOLCTTLTADVMSYIHSNMPALTEDMNGVPPPTSLVDY 417
      421 RPYOAVITCQKDAAPENKDPYDKLTFMNVDLKEKFSLDLDQYPLGKRFVLQAGLRKP 480
      418 RPYTSQAITCQKTAPOKPKEDPKDYFVFNKKEKFSADLDQPLGKRFVLQAGLRAR 477
      481 TIGPKRSAPSATSSKPAKRVYR 505
      478 KFKARNSAPASSTTT-PAKRRKTK 502

```

RESULT 13

```

LI protein - human papillomavirus type 51
C:Species: human papillomavirus type 51
A:Note: host Homo sapiens (man)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: G40415; G44889
R:lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A:Title: Biologic properties and nucleotide sequence analysis of human papillomavirus
A:Reference number: A40415; M0ID:91303675; PMID:1649326
A:Accession: G40415
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-504 <LUN>
A:Cross-references: GB:M62877
R:van den Brule, A.J.; Snijders, P.J.; Raaphorst, P.M.; Schrijnemakers, H.F.; Delius,
J. Clin. Microbiol. 30, 1716-1721, 1992
A:Title: General primer polymerase chain reaction in combination with sequence analysis
A:Reference number: A44889; M0ID:92332706; PMID:1321168
A:Accession: G44889
A:Molecule type: DNA
A:Residues: 337-369 <VAN>
A:Cross-references: GB:S40272; NID:g251694; PIDN:AAB22568.1; PID:g251695
A:Experimental source: mucosotropic type 51, cervical smear
A:Note: sequence extracted from NCBI backbone (NCBIN:109397, NCBI:P.109409)
C:Superfamily: papillomavirus LI protein
C:Keywords: late protein

```

```

Query Match      66.0%; Score 1804.5; DB 1; Length 504;
Best Local Similarity 64.0%; Pred. No. 4.8e-138;
Matches 323; Conservative 83; Mismatches 96; Indels 3; Gaps 3;

      1 MALWRPSDNTVYLPSPSVARVNTDVTYRTSIFHYAGSSRLTLVGNPFRVPAGGKNQ 60
      1 MALMRNDKSVYLPSPSVKVSSTDEVYRTNITYHAGSSRLTLVGNPFRVPAGGKNQ 60
      61 DIRKVSAYQYRVRRVQLDPDNKFGLPDINSIYNPETORLVACAGVEIGRQPLGVLGSH 120
      61 AIPKVSAYQYRVRRVQLDPDNKFGLPDINSIYNPETORLVACAGVEIGRQPLGVLGSH 119
      121 PFYNNKLDDESSHAATSNVEDYRVNVDYKOTQLCTICAPALGHNKGTACKSRPL 180
      121 PLFNKDDTENSRLANGNAQGVDRMTSYDNKOTQLCTICAPALGHNKGTACKSRPL 179
      181 SGGDPPPLELKTNYLEDGMVDTGYGAMDFSTLDQTKCEVPDLCOSICKYDYLOMSAD 240
      181 PBDGCPPLELKTNYLEDGMVDTGYGAMDFSTLDQTKCEVPDLCOSICKYDYLOMSAD 239
      241 PYGDSMFFCLRRQDLFARHFNWAGTMDGTPOSILYKGTGKARASPGSCVSPSPSGT 299
      240 TYGNSMFFCLRRQDLFARHFNWAGTMDGTPOSILYKGTGKARASPGSCVSPSPSGT 299
      300 VTSDSOLFENKPYLHRAQGNNGICWNOLFTVYVDTTRSTNLTICASTOSPPVPGQYAT 359
      300 ITSDSOLFENKPYLHRAQGNNGICWNOLFVTVVDTTRSTNLTICASTOSPPVPGQYAT 358
      360 KFKOYSHVEYDLOLTFOLCTTLTADVMSYIHSNNSLTEDMNGVPPPTSLVDY 419

```

Db 359 NRQYIRHGEVEYELQIFOLCKITLTTEVMAIHTMDPTITLQMNNGTLPPSASIEDAY 418
 QY 420 REVQSVATTCORDAAPAEKNDPYDKLFKNVNDLKEKESLDLDQYPLGRFFLYOAGLRKP 479
 Db 419 RFRVNAATSCQCKDTPQAKDPDLAKYKFNVDLKEKESLDLDQFALGRFFLYOAGLRKP 478
 QY 480 TIGPKRRSAPSAATSSKPAKRV 504
 Db 479 RPLKRRPASSASSSSSSAKRRVK 503

RESULT 14

PLWLS8
 L1 protein - human papillomavirus type 58
 C:Species: human papillomavirus type 58
 A:Note: host Homo sapiens (man)
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jul-2000
 C:Accession: G36779
 R:Kiriil, Y.; Iwamoto, S.; Matsukura, T.
 Virology 185, 424-427, 1991
 A:Title: Human papillomavirus type 58 DNA sequence.
 A:Reference number: A36779; MUID:92024102; PMID:1656594
 A:Accession: G36779
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-524 <KIR>
 A:Cross-references: GB:D90400; NID:9222386; PIDN:BA31851.1; PID:9337104
 C:Superfamily: papillomavirus L1 protein
 C:Keywords: late protein

Query Match 66.0%; Score 1804.5; DB 1; Length 524;
 Best Local Similarity 65.0%; Pred. No. 5,1e-138;
 Matches 327; Conservative 73; Mismatches 96; Indels 7; Gaps 4;

QY 1 MALMRSDNTVYLPPPSVAVVNTDDYVRTSTFYHAGSSRLTGVNPFYRVDPAGGQNO 60
 Db 27 MSVWRSEATVYLPVPVSKVSTDEYVRSITYYAGSSRLLAGNPFYSIKSPNNKK 86
 QY 61 D-IPRVSAYQYVFRVQLDPNKGFLPONSISYNETQRLVMACAGVEIGRQPLGVLSG 119
 Db 87 YVAPKVSGLQYVFRVRLDPNKGFLPONSISYNETQRLVMACAGVEIGRQPLGVLSG 146
 QY 120 HPEYKRLDPTSSHAATSNVSEDVYRDNVVDYKQOTLCILGAPAIQEMAKGTACKSRP 179
 Db 147 HPEYKRLDPTSSHAATSNVSEDVYRDNVVDYKQOTLCILGAPAIQEMAKGTACKSRP 206
 QY 180 LSGQDCPPLKNTLVLEDGMVDTGYGAMDFSTLDTCCEVPLDQCISICKYPDYQMSA 239
 Db 207 AAT-DQPLKELNLSIEDGMVDTGYGAMDFSTLDTCCEVPLDQCISICKYPDYQMSA 265
 QY 240 DRYGDSMEFLARQELFAHFHNNRAGTMDVTPQSLYIKGTGNRASPGSCVYSPSPSGSI 299
 Db 266 ERYGDSMEFLARQELFAHFHNNRAGTMDVTPQSLYIKGTGNRASPGSCVYSPSPSGSI 325
 QY 300 VNSDSOLFNRKPYMLHKAQGHNNIGCHNOLFVTVDTSTNTLTICASQSPVPGYDMF 359
 Db 326 VNSDSOLFNRKPYMLHKAQGHNNIGCHNOLFVTVDTSTNTLTICASQSPVPGYDMF 383
 QY 360 KFRQYSRHYEYDLQIFOLCTITTLADVMYSIHNSNISLEDNMGVPPPTSLVDYK 419
 Db 384 NKREYVRHYEYDLQIFOLCTITTLAEIMTYIHTMDSNILEDMOGGLPPSASISQDYK 443
 QY 420 REVQSVATTCORDAAPAEKNDPYDKLFKNVNDLKEKESLDLDQYPLGRFFLYOAGLRKP 479
 Db 444 RFTVSQATTCQKADPDLAKYKFNVDLKEKESLDLDQFALGRFFLYOAGLRKP 503
 QY 480 TIGPKRRSAPSAATSSKPAKRV 502
 Db 504 RL---KRSAPITRAPSTKRRKKV 523

RESULT 15
 S36578

L1 protein - human papillomavirus type 52
 C:Species: human papillomavirus type 52
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S36578; I44889
 R:Deilus, H.; Hofmann, B.
 Submitted to the EMBL Data Library, August 1993
 A:Description: Primer-directed sequencing of human papillomavirus types.
 A:Reference number: S36469
 A:Accession: S36578
 A:Molecule type: DNA
 A:Residues: 1-529

A:Cross-references: EMBL:X74481; NID:9397038; PIDN:CA52590.1; PID:9397045
 R:van den Brule, A.J.; Snijders, P.J.; Raaphorst, P.M.; Schilfinkemakers, H.F.; Deilus, J. Clin. Microbiol. 30, 1716-1721, 1992
 A:Title: General primer polymerase chain reaction in combination with sequence analysis
 A:Reference number: A44889; MUID:92332706; PMID:1321168
 A:Accession: I44889
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 368-399 <VAN>
 A:Cross-references: GB:S40277; NID:9251698; PIDN:AA22570.1; PID:9251699
 A:Experimental source: type Xa, cervical carcinoma in situ
 A:Note: sequence extracted from NCBI backbone (NCBI:109399, NCBI:109447)
 C:Superfamily: papillomavirus L1 protein
 C:Keywords: late protein

Query Match 65.9%; Score 1801.5; DB 2; Length 529;
 Best Local Similarity 65.0%; Pred. No. 9e-138;
 Matches 328; Conservative 69; Mismatches 101; Indels 7; Gaps 3;

QY 1 MALMRSDNTVYLPPPSVAVVNTDDYVRTSTFYHAGSSRLTGVNPFYRV---PAGG 57
 Db 27 MSVWRSEATVYLPVPVSKVSTDEYVRSITYYAGSSRLTGVNPFYSIKNTSSGNG-86
 QY 58 NKQDVKVSAYQYVFRVQLDPNKGFLPONSISYNETQRLVMACAGVEIGRQPLGVLSG 117
 Db 87 KVLVPRVSGLOQYVFRVRLDPNKGFLPONSISYNETQRLVMACAGVEIGRQPLGVLSG 146
 QY 118 SGHPEYKRLDPTSSHAATSNVSEDVYRDNVVDYKQOTLCILGAPAIQEMAKGTACKSRP 177
 Db 147 SGHPEYKRLDPTSSHAATSNVSEDVYRDNVVDYKQOTLCILGAPAIQEMAKGTACKSRP 206
 QY 178 RPLSGDCPPLKNTLVLEDGMVDTGYGAMDFSTLDTCCEVPLDQCISICKYPDYQMSA 237
 Db 207 NSGNPDCPPLKNTLVLEDGMVDTGYGAMDFSTLDTCCEVPLDQCISICKYPDYQMSA 266
 QY 238 SADPYGDSMEFLARQELFAHFHNNRAGTMDVTPQSLYIKGTGNRASPGSCVYSPSPSGSI 295
 Db 267 ASEPYGDSMEFLARQELFAHFHNNRAGTMDVTPQSLYIKGTGNRASPGSCVYSPSPSGSI 326
 QY 326 VNSDSOLFNRKPYMLHKAQGHNNIGCHNOLFVTVDTSTNTLTICASQSPVPGYDMF 355
 Db 356 VNSDSOLFNRKPYMLHKAQGHNNIGCHNOLFVTVDTSTNTLTICASQSPVPGYDMF 384
 QY 385 YKNEKEKYLRLHGEEDLQIFOLCTITTLADVMYSIHNSNISLEDNMGVPPPTSLVDYK 415
 Db 416 YKNEKEKYLRLHGEEDLQIFOLCTITTLADVMYSIHNSNISLEDNMGVPPPTSLVDYK 444
 QY 445 EDYRFTVSQATTCQKADPDLAKYKFNVDLKEKESLDLDQYPLGRFFLYOAGLRKP 475
 Db 476 EDYRFTVSQATTCQKADPDLAKYKFNVDLKEKESLDLDQYPLGRFFLYOAGLRKP 504
 QY 505 QARPKLRPASSAPSTSTKRRKKV 529

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OM protein - protein search, using sw model

Run on: October 17, 2003, 10:55:49 ; Search time 25.7169 Seconds
(without alignments)
1723.913 Million cell updates/sec

Title: US-08-913-644-4

Perfect score: 2405
Sequence: 1 MWSHRAARRKRAVTDLYKT.....FIPKRRKRVPEFADGFVAA 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2317.5	96.4	462	1 P2WL18	L2 protein - human
2	1973	82.0	463	2 S36565	L2 protein - human
3	1716	71.4	469	1 P2WLPR	L2 protein - human
4	1686.5	70.1	470	1 P2WL39	L2 protein - human
5	1532.5	63.7	470	2 S36536	L2 protein - human
6	1530	63.6	463	2 S36507	L2 protein - human
7	1529	63.6	463	2 S36530	L2 protein - human
8	1513	62.9	473	2 S36553	L2 protein - human
9	1486.5	61.8	464	2 S36582	L2 protein - human
10	1483.5	61.7	472	2 S36548	L2 protein - human
11	1466.5	61.0	468	1 P2WL51	L2 protein - human
12	1457	60.6	524	1 S15619	L2 protein - human
13	1423.5	59.2	464	2 S36501	L2 protein - human
14	1387.5	57.7	465	1 S15626	L2 protein - human
15	1164.5	48.4	466	1 P2WL31	L2 protein - human
16	1158	48.1	463	1 P2WL13	L2 protein - human
17	1149.5	47.8	455	1 P2WL11	L2 protein - human
18	1138.5	47.3	466	1 P2WL11	L2 protein - human
19	1133.5	47.1	466	2 S36577	L2 protein - human
20	1133.5	47.1	473	1 P2WLHS	minor capsid prote
21	1131	47.0	459	1 P2WL6	L2 protein - human
22	1117	46.4	477	1 P2WL42	L2 protein - human
23	1116.5	46.4	472	1 P2WL58	L2 protein - human
24	1114	46.3	467	1 P2WL33	L2 protein - human
25	1110	46.2	463	1 P2WL31	L2 protein - human
26	1108.5	46.1	456	2 S36588	L2 protein - human
27	1088	45.2	472	2 S36519	L2 protein - human
28	1087.5	45.2	476	2 S36513	L2 protein - human
29	1069	44.4	467	2 S36559	L2 protein - human

30	1060	44.1	469	2 S36525	L2 protein - human
31	1053	43.8	469	1 P2WL35	L2 protein - human
32	642.5	26.7	519	2 S36471	L2 protein - human
33	639.5	26.6	533	2 S36594	L2 protein - human
34	628.5	26.1	533	2 S36477	L2 protein - human
35	627	26.1	492	1 P2WL47	L2 protein - human
36	625	26.0	518	1 P2WL47	L2 protein - human
37	621	25.8	518	1 P2WL47	L2 protein - human
38	620.5	25.8	520	2 S36489	L2 protein - human
39	608.5	25.3	520	2 S36495	L2 protein - human
40	606	25.2	518	1 P2WL5	L2 protein - human
41	604.5	25.1	524	2 S36483	L2 protein - human
42	597	24.8	518	2 S36542	L2 protein - human
43	591.5	24.6	521	2 S36571	L2 protein - human
44	586	24.4	518	1 P2WL8	L2 protein - human
45	574	23.9	507	1 P2WL	L2 protein - human

ALIGNMENTS

RESULT 1

L2 protein - human papillomavirus type 18

C/Species: human papillomavirus type 18

C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999

C/Accession: B26251

R/Col: S.T.; Danos, O.

J. Mol. Biol. 193, 599-608, 1987

A/Title: Nucleotide sequence and comparative analysis of the human papillomavirus typ

A/Reference number: A92937; MUID:87283882; PMID:3039146

A/Accession: B26251

A/Molecule type: DNA

A/Residues: 1462 <COL>

A/Cross-references: GB:X05015; NID:960975; PIDN:CAA28670.1; PID:960982

C/Superfamily: papillomavirus L2 protein

C/Keywords: late protein

Query Match 96.4% Score 2317.5; DB 1; Length 462;
Best Local Similarity 96.8%; Pred. No. 1.6e-130;
Matches 447; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY	1	MWSHRAARRKRAVTDLYKTCKOSGTCPSDVVKVGGTTLADKILLOMSSLGITLGLGIG	60
DB	1	MWSHRAARRKRAVTDLYKTCKOSGTCPPVVKVGGTTLADKILLOMSSLGITLGLGIG	60
QY	61	TGSGTGRTGYIPLGGRSNTVDVGPTRPVVIEVGPPTDPSIVTLIEDSVVTSGAPRP	120
DB	61	TGSGTGRTGYIPLGGRSNTVDVGPTRPVVIEVGPPTDPSIVTLIEDSVVTSGAPRP	120
QY	121	TFTGTSGFDITSGTTPAVLDITPSSSTVSTTNFTNPAFSDPSIIIEVPOGEVAGNV	180
DB	121	TFTGTSGFDITSGTTPAVLDITPSSSTVSTTNFTNPAFSDPSIIIEVPOGEVAGNV	180
QY	181	FVGTPTSGTHGYEIEIQLTFEASSGTGCEEPISPLPTVRRVACPRISRAYOQVSANPE	240
DB	181	FVGTPTSGTHGYEIEIQLTFEASSGTGCEEPISPLPTVRRVACPRISRAYOQVSANPE	240
QY	241	FLTRPSSLTYDNPAPPEVDVTLTFEPRSNVPSDPMIDILRLRPALTSRGRVRSRLG	300
DB	241	FLTRPSSLTYDNPAPPEVDVTLTFEPRSNVPSDPMIDILRLRPALTSRGRVRSRLG	300
QY	301	QRATMTFRSGTOIGAVVHYHDSPLAPSEVIEIQLPVASATDNGLFDIYADDIDPAMP	360
DB	301	QRATMTFRSGTOIGAVVHYHDSPLAPSEVIEIQLPVASATDNGLFDIYADDIDPAMP	360
QY	361	VPSRPTTSAAVSTYSPTISSASSYSNVTVPLTSSMDVPYVTGPDITLP-PTSWPITVSP	419
DB	361	VPSRPTTSAAVSTYSPTISSASSYSNVTVPLTSSMDVPYVTGPDITLP-PTSWPITVSP	419
QY	420	APASTOYIGIHGTHYIPLPLYYFIPKRRKRVPEFADGFVAA 461	
DB	421	APASTOYIGIHGTHYIPLPLYYFIPKRRKRVPEFADGFVAA 462	

RESULT 2
S36565
L2 protein - human papillomavirus type 45
C:Species: human papillomavirus type 45
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S36565
R:Delius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36565
A:Molecule type: DNA
A:Residues: 1-463
A:Cross-references: EMBL:X74479; NID:g937022; PIDN:CAA52577.1; PID:g937028
C:Superfamily: papillomavirus L2 protein
C:Keywords: late protein

Query Match 82.0%; Score 1973; DB 2; Length 463;
Best Local Similarity 81.7%; Pred. No. 4.8e-110;
Matches 379; Conservative 33; Mismatches 48; Indels 4; Gaps 3;

```

OY 1 MSHRAARRKASVTDLYKTCCKOSGTCPSDVNKEGTTLADKTLQWSSLGIFLGIG 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSHRAARRKASVTDLYKTCCKOSGTCPPVYNKEGTTLADKTLQWSSLGIFLGIG 60

OY 61 TSGGTGRTGYIPLGGRSNTVDVGPTRPVVIEPVGPTDPSIYTLIEDSSVVTSGARP 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TSGSGGRTGYVPLGGRSNTVDVGPTRPVVIEPVGPTDPSIYTLIEDSSVVTSGARP 120

OY 121 TFGTSGFDITSAGTTTTPAVLDITPSSVSISTNTNTNPAFSPDPIIEVPQGEVGNV 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TFGTSGFEITSSSTTTPAVLDITPSSVSISTNTNTNPAFSDPIIEVPQGEVGNV 180

OY 121 TFGTSGFEITSSSTTTPAVLDITPSSVSISTNTNTNPAFSDPIIEVPQGEVGNV 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TFGTSGFEITSSSTTTPAVLDITPSSVSISTNTNTNPAFSDPIIEVPQGEVGNV 180

OY 181 FVGTPTGTGHEIEIPLQTRASSSGTEEPISSTPLPVRRVAGRLYSRAVQVSVANPE 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 FVGTPTGTGHEIEIPLQTRASSSGTEEPISSTPLPVRRVAGRLYSRAVQVSVANPE 240

OY 181 FVGTPTGTGHEIEIPLQTRASSSGTEEPISSTPLPVRRVAGRLYSRAVQVSVANPE 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 FVGTPTGTGHEIEIPLQTRASSSGTEEPISSTPLPVRRVAGRLYSRAVQVSVANPE 240

OY 241 FLTRPSSLITYDNPAPFVPDITLFEPRSNVPSDEMDIIRLHRPALTSRRGTVRSRLG 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 FLTRPSSLITYDNPAPFVPDITLFEPRSNVPSDEMDIIRLHRPALTSRRGTVRSRLG 300

OY 301 ORATMTFRSGTQIGARVHFHNDISPIAPSEYEIQLPLVNSTENGFLDIADIDIDAMP 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 ORATMTFRSGTQIGARVHFHNDISPIAPSEYEIQLPLVNSTENGFLDIADIDIDAMP 360

OY 301 ORATMTFRSGTQIGARVHFHNDISPIAPSEYEIQLPLVNSTENGFLDIADIDIDAMP 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 ORATMTFRSGTQIGARVHFHNDISPIAPSEYEIQLPLVNSTENGFLDIADIDIDAMP 360

OY 361 VPSRPTTSSAVSYSPYSS--ASSYSANVTVPLTSSMDVPVYTGPDITLPP--TSVMPYVS 417
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 360 TPTSTHNSFTYRKSLTMTPTAASSYSNVTVPPLTSSMDVPVYTGPDITLPP--TSVMPYVS 419

OY 418 PTAPASTQYIGHGHYIYLPYLFYIPKRRKRVYEFADGFVA 461
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 420 PTNASTTWTYIGHGHYIYLPYLFYIPKRRKRVYEFADGFVA 463

```

RESULT 3

P2MWLPR
L2 protein - human papillomavirus type ME180 (provirus)
C:Species: human papillomavirus type ME180
A:Note: host Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 28-Jul-2000
C:Accession: A40509
R:Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma
A:Reference number: A40509; MUID:91374616; PMID:1716694
A:Accession: A40509
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-469 <REU>
A:Cross-references: GB:M73258; NID:g184383; PIDN:AAFL14009.1; PID:g6478869
C:Superfamily: papillomavirus L2 protein

C:Keywords: late protein

Query Match 71.4%; Score 1716; DB 1; Length 469;
Best Local Similarity 70.1%; Pred. No. 8.9e-95;
Matches 329; Conservative 62; Mismatches 68; Indels 10; Gaps 4;

```

OY 1 MSHRAARRKASVTDLYKTCCKOSGTCPSDVNKEGTTLADKTLQWSSLGIFLGIG 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSHRAARRKASVTDLYKTCCKOSGTCPPVYNKEGTTLADKTLQWSSLGIFLGIG 60

OY 61 TSGGTGRTGYIPLGGRSNTVDVGPTRPVVIEPVGPTDPSIYTLIEDSSVVTSGARP 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TSGSGGRTGYIPLGGRSNTVDVGPTRPVVIEPVGPTDPSIYTLIEDSSVVTSGARP 120

OY 121 TFGTSGFDITSAGTTTTPAVLDITPSSVSISTNTNTNPAFSPDPIIEVPQGEVGNV 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TFGTSGFEITSSSTTTPAVLDITPSSVSISTNTNTNPAFSDPIIEVPQGEVGNV 180

OY 121 TFGTSGFEITSSSTTTPAVLDITPSSVSISTNTNTNPAFSDPIIEVPQGEVGNV 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TFGTSGFEITSSSTTTPAVLDITPSSVSISTNTNTNPAFSDPIIEVPQGEVGNV 180

OY 181 FVGTPTGTGHEIEIPLQTRASSSGTEEPISSTPLPVRRVAGRLYSRAVQVSVANPE 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 FVGTPTGTGHEIEIPLQTRASSSGTEEPISSTPLPVRRVAGRLYSRAVQVSVANPE 240

OY 241 FLTRPSSLITYDNPAPFVPDITLFEPRSNVPSDEMDIIRLHRPALTSRRGTVRSRLG 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 FLTRPSSLITYDNPAPFVPDITLFEPRSNVPSDEMDIIRLHRPALTSRRGTVRSRLG 300

OY 301 ORATMTFRSGTQIGARVHFHNDISPIAPSEYEIQLPLVNSTENGFLDIADIDIDAMP 357
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 ORATMTFRSGTQIGARVHFHNDISPIAPSEYEIQLPLVNSTENGFLDIADIDIDAMP 359

OY 358 AMPVP-----SRPTSSAVSYSPYSS--ASSYSANVTVPLTSSMDVPVYTGPDITLPP 412
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 360 TTVLDTRAFHNAFTSRSHISVPSLASASTYATNTIPIGTANMTPTNTGPDVLTPTSP 419

OY 413 WPIYSPAPASTQYIGHGHYIYLPYLFYIPKRRKRVYEFADGFVA 460
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 420 QLPFTPTPTDITTYAITTYGNTYLLPLFLFKKRRRLYFPADGIVA 468

```

RESULT 4

P2MWL39
L2 protein - human papillomavirus type 39
C:Species: human papillomavirus type 39
A:Note: host Homo sapiens (man)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C:Accession: G38502
R:Volpers, C.; Strebeck, R.E.
Virolgy 181, 419-423, 1991
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A:Reference number: A38502; MUID:91135017; PMID:1847286
A:Accession: G38502
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-470 <VOL>
A:Cross-references: GB:M62849; EMBL:M38185; NID:g333245; PIDN:AAA4705.1; PID:g463191
C:Superfamily: papillomavirus L2 protein
C:Keywords: late protein

Query Match 70.1%; Score 1686.5; DB 1; Length 470;
Best Local Similarity 69.6%; Pred. No. 5e-93;
Matches 328; Conservative 60; Mismatches 70; Indels 13; Gaps 7;

```

OY 1 MSHRAARRKASVTDLYKTCCKOSGTCPSDVNKEGTTLADKTLQWSSLGIFLGIG 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSHRAARRKASVTDLYKTCCKOSGTCPPVYNKEGTTLADKTLQWSSLGIFLGIG 60

OY 61 TSGGTGRTGYIPLGGRSNTVDVGPTRPVVIEPVGPTDPSIYTLIEDSSVVTSGARP 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TGTGTGRTGYIPLGGRSNTVDVGPTRPVVIEPVGPTDPSIYTLIEDSSVVTSGARP 120

OY 121 TFGTSGFDITSAGTTTTPAVLDITPSSVSISTNTNTNPAFSPDPIIEVPQGEVGNV 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TFGTSGFEITSSSTTTPAVLDITPSSVSISTNTNTNPAFSDPIIEVPQGEVGNV 180

```

```

QY      181 FVCTPTSGTHGYEIEIPLQTFASSGTGCEPISSTPLPTVRRVACPRLYSRAVQOVSVANPE 240
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 FVSTPTSGTHGYEIEIPEWEFATGCTGTEPISSTPTGKISRAGPRLYSRAHQOVRSNFD 240
QY      244 FLTRPSSLLTYDNPAPPEVDLTTLTFEPRSNVPPSDMDIIRLRPALTSRGRVRSRLG 300
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      244 FVTHSSFTYEDNPAPEPDDTLTLTEADIAIDPDLDVLRHLRPAITSRGTGVRSLG 300
QY      301 ORATMFTRSQTQIGARVHFYHDISPIAPSEYIELOPLVSA---TEDNGLFDIYAD-DID 356
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301 KKATMTTRGTOIGAVHYHDISSIAPA-ESTELQPLVAEESDASDALFDIYADVDDN 359
QY      357 PAMPVPSRPTTSSAVSTYS---PTSSASS--YSNVVPLTSSMDVPVYTGPDITLPT 410
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      360 TYLDTAFFNNTROSG-PTYNNGSLPVSASSASTKYANTWTIPSTSMNMPVNTGDIALPST 418
QY      411 SWMPIVSPAPASTOY-IGIGHYHYLMPLYEIPKRRKRVPEFADGFA 460
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      419 TPOLPLVPSGPDITTYAITIGSGNYLLPLLYFLKRRKRIPEFSDGYA 469

```

RESULT 5

```

S36536
L2 protein - human papillomavirus type 10
C:Species: human papillomavirus type 10
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S36536
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36536
A:Molecule type: DNA
A:Residues: 1-470 <DEL>
A:Cross-references: EMBL:X74465; NID:g396901; PIDN:CAA52493.1; PID:g396907
C:Superfamily: papillomavirus L2 protein
C:Keywords: late protein

```

```

Query Match      63.7%; Score 1532.5; DB 2; Length 470;
Best Local Similarity 63.9%; Pred. No. 7,1e-84;
Matches 301; Conservative 69; Mismatches 88; Indels 13; Gaps 9;

```

```

QY      1 MNSHRAARRRASVTDLYKTCOSGTCPSDVNKKVEGTTLADKILQWSSLGIFLGIGIG 60
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MVAORARRRRKASATOLYKTCASGTCPPDVIPKVGSTLADRILOMGSLGYVIGLGIG 60
QY      61 TSGGTGRTGYIPLGGRSMYVDVG--PTRRPVYIEVGPPTDPSITVLIEDSSVYTGAPR 119
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 TSGGTGRTGYIPLGGRSMYVDVG--PTRRPVYIEVGPPTDPSITVLIEDSSVYTGAPR 119
QY      120 PTFVGTSGFDITSGATTTPAVLDITPSSVSISTNTNPAFSDSIIEVPOTGEVSGN 179
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 PTFSGTSGFEVTSATTTTAVLDITPASEVNVISSTNFINPATRESLVEVPSGEGVSGH 180
QY      180 VEVGTPTSGTHGYEIEIPLQTFASSGTGCEPISSTPLPTVRRVACPRLYSRAVQOVSVANPE 239
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 ILISTPTAGTHGYEIEIPEWEFATGCTGTEPISSTPTGKISRAGPRLYSRAHQOVRSNFD 240
QY      240 EFLTRPSSLLTYDNPAPPEVDLTTLTE---PRSNVPSDDMDIIRLRPALTSRGRVRSRLG 296
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 AFLTRPSSLLTYDNPAPPEVDLTTLTE---PRSNVPSDDMDIIRLRPALTSRGRVRSRLG 300
QY      297 SRLGORATMFTRSQTQIGARVHFYHDISPIAPSEYIELOPLVSAEDNGLFDIYAD-DID 354
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301 SRLGOKFSMKRISRGKIGARVHYHDISSIAPA-EDIEKEPLIAPAASDIYIIFADVDD 359
QY      355 IDPAMPVPSRPTTSS-AVSTYSPTISSASS-YSNVVPLTSSMDVPVYTGPDITLPTSY 412
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      360 GIVAFEGYRSTOSGMYNTSPLSTLSTKYGNVMIPEVSPVDVLRHLRPAITSRGTGVRSLG 419
QY      413 WPIVSPITAPA-SNOYIGIGHYHYLMPLYEIP-KKRRKRVPEFADGFA 460
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

Db      420 WPIVSPITADTHYIYIDGGDFYLMPEVTEHFSNRHRRKRVSYFFADGTLLA 469

```

RESULT 6

```

S36507
L2 protein - human papillomavirus type 30
C:Species: human papillomavirus type 30
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S36507
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36507
A:Molecule type: DNA
A:Residues: 1-463 <DEL>
A:Cross-references: EMBL:X74474; NID:g396973; PIDN:CAA52547.1; PID:g396979
C:Superfamily: papillomavirus L2 protein
C:Keywords: late protein

```

```

Query Match      63.6%; Score 1530; DB 2; Length 463;
Best Local Similarity 63.2%; Pred. No. 9,7e-84;
Matches 295; Conservative 68; Mismatches 94; Indels 10; Gaps 8;

```

```

QY      1 MNSHRAARRRASVTDLYKTCOSGTCPSDVNKKVEGTTLADKILQWSSLGIFLGIGIG 60
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MVAHRAARRRRKASATOLYKTCQKANGCPSDVINKIEHTTLADKILQMGSLFTFFGNLGIG 60
QY      61 TSGGTGRTGYIPLGGRSMYVDVGPRRPVYIEVGPPTDPSITVLIEDSSVYTGAPR 120
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 TGAGSGGRAGYVPLGTPTTVVDSAPRPVIESVGPDPDPSITVLIEDSSVYVAGASFP 120
QY      121 TPTGTSGFDITSGATTTPAVLDITPSSVSISTNTNPAFSDSIIEVPOTGEVSGN 180
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 NPTGTAGFEVTSSTTTTAVLDITPTTGSHVSTHTNTNVEPPIEVIPQGEVSGHI 180
QY      181 FVCTPTSGTHGYEIEIPLQTFASSGTGCEPISSTPLPTVRRVACPRLYSRAVQOVSVANPE 240
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 LVSTPTSGVHSEIEIPEQTEAVAGTGEPISSPTPGLRIAPRILYQRAFGQVKTDP 240
QY      241 FLTRPSSLLTYDNPAPPEVDLTTLTFEPRSNVPPSDMDIIRLRPALTSRGRVRSRLG 300
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 FLTRPETLITVDNPEVADTLTLTFSSGVAAPDPEDLIYALRPAFTTTRGGRVRSRLG 300
QY      301 ORATMFTRSQTQIGARVHFYHDISPIAPSEYIELOPLVSAEDNGLFDIYAD-DIDPAM 359
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301 TKATMFTRSKQIGARVHYHDIYSPLAHTEE-IEMDPLSANNSPGLDITIA-NLDDEA 358
QY      360 PVPSSRPT--TSSAVSTYSPTISSASSYSNVTVPLTSSMDVPVYTGPDITLP--PTSWPI 415
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      359 PVSSHLSIAVPSRLPNTVPLSFSQNTVNTIPLGKMDVPIYSGPDIVLPCTPT-WP- 416
QY      416 VSTPTAASIOY-IGIGHYHYLMPLYEIPKRRKRVPEFADGFA 461
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      417 YAPQAPEDTTHVDVHIGSTFALMPVYVLRRRRRKHVYFLADGVA 463

```

RESULT 7

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S36530
L2 protein - human papillomavirus type 53
C:Species: human papillomavirus type 53
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S36530
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36530
A:Molecule type: DNA
A:Residues: 1-463 <DEL>
A:Cross-references: EMBL:X74482; NID:g397046; PIDN:CAA52594.1; PID:g397051
C:Superfamily: papillomavirus L2 protein
C:Keywords: late protein

```



```

Db      237 LVSTATSSHGEEELPMQTFATSGSGTEPISSTPLPGVRRVAGRLSRANQOQVNDP
      240 EELRPSLSITYNDPAPEVDITLFEPR-RSNVPSDMDIIRLRPALTSRGRVRSR 298
      297 AFLRPAALVTFDNPVYDPEETITFQHPDLHEPPDPDLVALHRLPALTSRGRVRSR 356
      299 LGRATMTSRSGTQIGARVHFYHDISPAPSPETIELOPLY-SATEDNG--LFDIYAD- 354
      357 LGRATMTSRSGTQIGARVHFYHDISPAPSPETIELOPLY-SATEDNG--LFDIYAD- 414
      355 -IDPAM-FVPSRPTSSAVSTYSPTISSASSY-SNVTYPLSSMDVPYTGPDITLPT- 410
      415 VLQPLDELPAAPRGSISLADYAVASASTLRSGTSTYLSGVDVPTGPDIE-PPNV 473
      411 -SVMPVSPAPASTQYIGIGHYHLYPLYYFLPKRRKRVYFFADGVAA 461
      474 PGMGPPLI-PVAPSLPSSVYIFGSDYILMPSTVLMKRRKRVHYFFADGVAA 524

```

RESULT 13

S36501
I2 protein - human papillomavirus type 27

C:Species: human papillomavirus type 27

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S36501

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36501

A:Molecule type: DNA

A:Residues: 1-464

A:Cross-references: EMBL:X74473; NID:g396964; PIDN:CAA52540.1; PID:g396970

C:Superfamily: papillomavirus I2 protein

C:Keywords: late protein

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Query Match      59.2%; Score 1423.5; DB 2; Length 464;
Best Local Similarity 60.1%; Fred. No. 2.1e-77;
Matches 283; Conservative 70; Mismatches 95; Indels 23; Gaps 11;

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      5 RAARRKASVTDLYTKCKSGTCDVYNNKVEGTILAKIILQMSLGIFLGIGTSG 64
      3 RAKRRKRASPTDLYTKCKAGTCCPDITLRLQNTLADKILKMSLGIFFGGLGIGTSG 62
      65 TCGRTGYIPLGGRSNTVDVG-PRRPVYIEPVGPTDPSIYTLIEDSSVTSAGAPRPT 123
      63 TGGRTGYIPLGGRSNTVDVG-PRRPVYIEPVGPTDPSIYTLIEDSSVTSAGAPRPT 122
      124 GTSGPDITSAGTTTAVADITPSSSVSISTNTFNPAFSDPSITIEVQTEGVSQNVYV 183
      123 GTGGEVTTSTVTPDAVIDITPSSSVSISTNTFNPAFSDPSITIEVQTEGVSQNVYV 182
      184 TPTSGTHGYEELPLOTFASS-GTGEPISSPTLPVRRVAGPRLYSRAVQVSVANPEL 242
      183 TATSGSHGYEELPLOTFASS-GTGEPISSPTLPVRRVAGPRLYSRAVQVSVANPEL 242
      243 TRPSLSITYNDPAPEVDITLFEPR-SNVPSDMDIIRLRPALTSRGRVRSR 301
      243 ERPADLVTFDNPVYDPEETITFQHPDLHEPPDPDLVALHRLPALTSRGRVRSR 302
      302 RATMTSRSGTQIGARVHFYHDISPAPSPETIELOPLY-SATEDNG--LFDIYAD- 353
      303 RATMTSRSGTQIGARVHFYHDISPAPSPETIELOPLY-SATEDNG--LFDIYAD- 360
      354 DIDPAMPVPSRPTSSAVSTYSPTISSASSY-SNVTYPLSSMDVPYTGPDITLPT- 410
      361 PLDDIYTPAPRGSISLADYAVASASTLRSGTSTYLSGVDVPTGPDIE-PPNV 414
      411 SVMPVSPAPASTQYIGIGHYHLYPLYYFLPKRRKRVYFFADGVAA 461
      415 GLGPLI-PVAPSLPSSVYIFGSDYILMPSTVLMKRRKRVHYFFADGVAA 464

```

RESULT 14

S15626
protein I2 - human papillomavirus type 57

C:Species: human papillomavirus type 57

A>Note: host Homo sapiens (man)

C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999

C:Accession: S15626

R:Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.

virus Res. 18, 81-98, 1990

A>Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a

A:Reference number: S15614; MUID:91186899; PMID:1964523

A:Accession: S15626

A:Molecule type: DNA

A:Residues: 1-465 <HIR>

A:Cross-references: EMBL:X55965; NID:960882; PIDN:CAA39435.1; PID:960888

C:Superfamily: papillomavirus I2 protein

C:Keywords: late protein

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Query Match      57.7%; Score 1387.5; DB 1; Length 465;
Best Local Similarity 59.8%; Fred. No. 2.8e-75;
Matches 284; Conservative 68; Mismatches 98; Indels 25; Gaps 12;

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      2 VSHRAARRKASVTDLYTKCKSGTCDVYNNKVEGTILAKIILQMSLGIFLGIGT 61
      1 MSPRKRKRASPTDLYTKCKAGTCCPDITLRLQNTLADKILKMSLGIFFGGLGIGT 60
      62 GSGTGRGYIPLGGRSNTVDVG-PRRPVYIEPVGPTDPSIYTLIEDSSVTSAGAPR 120
      61 GSGTGRGYIPLGGRSNTVDVG-PRRPVYIEPVGPTDPSIYTLIEDSSVTSAGAPR 120
      121 TPTSGPDITSAGTTTAVADITPSSSVSISTNTFNPAFSDPSITIEVQTEGVSQNV 180
      121 TPTSGPDITSAGTTTAVADITPSSSVSISTNTFNPAFSDPSITIEVQTEGVSQNV 180
      121 TPTSGPDITSAGTTTAVADITPSSSVSISTNTFNPAFSDPSITIEVQTEGVSQNV 180
      181 FVGPPTSHTGYEELPLOTFASS-GTGEPISSPTLPVRRVAGPRLYSRAVQVSVANP 239
      181 LVSTATSSHGEEELPMQTFATSGSGTEPISSTPLPGVRRVAGRLSRANQOQVNDP 240
      240 EELRPSLSITYNDPAPEVDITLFEPR-RSNVPSDMDIIRLRPALTSRGRVRSR 297
      241 AFLRPAALVTFDNPVYDPEETITFQHPDLHEPPDPDLVALHRLPALTSRGRVRSR 300
      298 RLGORATMTSRSGTQIGARVHFYHDISPAPSPETIELOPLY-SATEDNG--LFDIYAD- 354
      301 RLGORATMTSRSGTQIGARVHFYHDISPAPSPETIELOPLY-SATEDNG--LFDIYAD- 357
      355 -IDPAMPVPSRPTSSAVSTYSPTISSASSY-SNVTYPLSSMDVPYTGPDITLPT- 406
      358 QPLSDVPAARRGITSLA-----DTAVASASTLRKATTPVLSGVDVPTGPDIDPS 412
      407 LPPTSVMPVSPAPASTQYIGIGHYHLYPLYYFLPKRRKRVYFFADGVAA 461
      413 VGP-GMGPPLI-PVAPSLPSSVYIFGSDYILMPSTVLMKRRKRVHYFFADGVAA 465

```

RESULT 15

P2ML31

I2 protein - human papillomavirus type 31

C:Species: human papillomavirus type 31

A>Note: host Homo sapiens (man)

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999

C:Accession: H32444

R:Goldsbrough, M.D.; Disilvestre, D.; Temple, G.F.; Iorincz, A.T.

Virology 171, 306-311, 1989

A>Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-as

A:Reference number: A94398; MUID:89299478; PMID:2545036

A:Accession: H32444

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-466 <GB>

A:Cross-references: GB:J04353; NID:g333048; PIDN:AAA46955.1; PID:g459921

C:Superfamily: papillomavirus I2 protein

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 17, 2003, 10:57:04 ; Search time 20.4783 Seconds
(without alignments)
952.486 Million cell updates/sec

Title: US-08-913-644-4

Perfect score: 2405

Sequence: 1 MWSHRARRRRKASVTDLTKT.....FIPKRRKRVYFFADGFVAA 461

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database: Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*\n2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*\n3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*\n4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*\n5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep:*\n6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2405	100.0	461	2	US-08-409-122-4
2	2405	100.0	461	2	US-08-408-669-4
3	2317.5	96.4	462	4	US-09-520-822A-4
4	1134	47.2	601	2	US-08-606-288-7
5	1134	47.2	601	2	US-08-606-288-10
6	1134	47.2	601	3	US-09-347-483-7
7	1134	47.2	601	3	US-09-347-483-10
8	1133.5	47.1	473	4	US-09-520-822A-2
9	1130.5	47.0	473	2	US-08-700-670A-23
10	408.5	17.0	469	4	US-09-479-645A-6
11	408.5	17.0	469	4	US-09-479-645A-8
12	380.5	15.8	964	4	US-08-484-791-2
13	151	6.3	878	4	US-09-556-706B-2
14	151	6.3	907	3	US-08-783-774-2
15	151	6.3	907	4	US-09-328-599A-1
16	151	6.3	907	5	PCT-US85-04611A-U9
17	148	6.2	2972	4	US-09-579-181-2
18	148	6.2	3118	4	US-09-579-181-1
19	145	6.0	2736	4	US-09-252-991A-30227
20	144.5	6.0	1537	1	US-08-325-267A-2
21	133	5.5	669	4	US-09-071-035-264
22	133	5.5	1638	4	US-09-071-035-258
23	133	5.5	1638	4	US-09-071-035-262
24	133	5.5	1638	4	US-09-071-035-266
25	131.5	5.5	941	4	US-07-757-022B-14
26	131.5	5.5	1022	4	US-07-757-022B-84
27	131.5	5.5	1038	4	US-07-757-022B-74

28	131.5	5.5	1049	4	US-07-757-022B-58	Sequence 58, App1
29	131.5	5.5	1140	4	US-07-757-022B-104	Sequence 104, App
30	131.5	5.5	1270	4	US-07-757-022B-44	Sequence 44, App1
31	131.5	5.5	1311	4	US-07-757-022B-42	Sequence 42, App1
32	131.5	5.5	1313	4	US-07-757-022B-142	Sequence 142, App
33	131.5	5.5	1314	4	US-07-757-022B-50	Sequence 50, App1
34	131.5	5.5	1320	4	US-07-757-022B-46	Sequence 46, App1
35	131.5	5.5	1354	4	US-07-757-022B-60	Sequence 60, App1
36	131.5	5.5	1361	4	US-07-757-022B-48	Sequence 48, App1
37	131.5	5.5	1363	4	US-07-757-022B-52	Sequence 52, App1
38	131.5	5.5	1404	4	US-07-757-022B-2	Sequence 2, App11
39	131.5	5.5	1404	4	US-07-757-022B-62	Sequence 62, App1
40	130	5.4	3892	4	US-09-328-352-5503	Sequence 5503, App
41	127	5.3	1132	4	US-09-198-452A-466	Sequence 466, App
42	126.5	5.3	1447	3	US-09-041-886-25	Sequence 25, App1
43	126.5	5.3	1447	5	PCT-US94-05277-2	Sequence 2, App11
44	126.5	5.3	1601	4	US-09-345-473E-40	Sequence 40, App1
45	126.5	5.3				

ALIGNMENTS

RESULT 1
US-08-409-122-4
Sequence 4, Application US/08409122
Patent No. 5820870
GENERAL INFORMATION:
APPLICANT: JOYCE, JAMES G.
APPLICANT: GEORGE, HUGH A.
APPLICANT: HOFMANN, KATHRYN J.
APPLICANT: JANSSEN, KATHRIN U.
APPLICANT: NEPPER, MICHAEL P.
TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE 18 VACCINE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Faststro Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,122
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/408,669
FILING DATE: 22-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19425
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-6734
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEetical: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:

US-08-409-122-4

Query Match 100.0%; Score 2405; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 7.3e-194;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSHRAARRKRASTYDLYKTKQSGTSPDVNKNVEGTTLADKILQMSLSLIGLIG 60
DB 1 MSHRAARRKRASTYDLYKTKQSGTSPDVNKNVEGTTLADKILQMSLSLIGLIG 60
QY 61 TSGGTGRTGYIPLGGRSNVVDVGPTRPPVIEPVGPTDPSITLLIEDSSVVTSGAPRP 120
DB 61 TSGGTGRTGYIPLGGRSNVVDVGPTRPPVIEPVGPTDPSITLLIEDSSVVTSGAPRP 120
QY 121 TFGTSGFDITSAGTTTPAVLDITPSSSTSVSISTNTNPAFSDPSIIEVPQGEVSGNV 180
DB 121 TFGTSGFDITSAGTTTPAVLDITPSSSTSVSISTNTNPAFSDPSIIEVPQGEVSGNV 180
QY 181 FVGPTSGTHGEIEIPLQTFASSGTGEPISSSTPLPVRRVAGRLYSRAVQVSVANPE 240
DB 181 FVGPTSGTHGEIEIPLQTFASSGTGEPISSSTPLPVRRVAGRLYSRAVQVSVANPE 240
QY 241 FLTRPSSLITYDNAPFEPVDITLFEPRSNVPSDFMDIIRLHRPALTSRGRVRSRLG 300
DB 241 FLTRPSSLITYDNAPFEPVDITLFEPRSNVPSDFMDIIRLHRPALTSRGRVRSRLG 300
QY 301 QRATMFTRSQTQICARVHFHDISPAPSPYIELQPLVSATENGLEFDIYADDIDPAMP 360
DB 301 QRATMFTRSQTQICARVHFHDISPAPSPYIELQPLVSATENGLEFDIYADDIDPAMP 360
QY 361 VPSRPTSSAVSTYSPITSSASSYSNTVPLTSSMDVPVYTGPDITLPPTSVMPVISP 420
DB 361 VPSRPTSSAVSTYSPITSSASSYSNTVPLTSSMDVPVYTGPDITLPPTSVMPVISP 420
QY 421 PASTQYIGIGHGTHYLLMPLYFFIPKRRKRVYFFADGFVAA 461
DB 421 PASTQYIGIGHGTHYLLMPLYFFIPKRRKRVYFFADGFVAA 461

RESULT 2

US-08-408-669-4
Sequence 4, Application US/08408669
Patent No. 5840306
GENERAL INFORMATION:
APPLICANT: HOEWANN, KATHRYN J.
APPLICANT: JANSEN, KATHRYN U.
APPLICANT: NEEBER, MICHAEL P.
TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE 18
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,669
FILING DATE: 22-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19424
TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-594-6734
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-408-669-4

Query Match 100.0%; Score 2405; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 7.3e-194;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSHRAARRKRASTYDLYKTKQSGTSPDVNKNVEGTTLADKILQMSLSLIGLIG 60
DB 1 MSHRAARRKRASTYDLYKTKQSGTSPDVNKNVEGTTLADKILQMSLSLIGLIG 60
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DB 61 TSGGTGRTGYIPLGGRSNVVDVGPTRPPVIEPVGPTDPSITLLIEDSSVVTSGAPRP 120
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DB 121 TFGTSGFDITSAGTTTPAVLDITPSSSTSVSISTNTNPAFSDPSIIEVPQGEVSGNV 180
QY 181 FVGPTSGTHGEIEIPLQTFASSGTGEPISSSTPLPVRRVAGRLYSRAVQVSVANPE 240
DB 181 FVGPTSGTHGEIEIPLQTFASSGTGEPISSSTPLPVRRVAGRLYSRAVQVSVANPE 240
QY 241 FLTRPSSLITYDNAPFEPVDITLFEPRSNVPSDFMDIIRLHRPALTSRGRVRSRLG 300
DB 241 FLTRPSSLITYDNAPFEPVDITLFEPRSNVPSDFMDIIRLHRPALTSRGRVRSRLG 300
QY 301 QRATMFTRSQTQICARVHFHDISPAPSPYIELQPLVSATENGLEFDIYADDIDPAMP 360
DB 301 QRATMFTRSQTQICARVHFHDISPAPSPYIELQPLVSATENGLEFDIYADDIDPAMP 360
QY 361 VPSRPTSSAVSTYSPITSSASSYSNTVPLTSSMDVPVYTGPDITLPPTSVMPVISP 420
DB 361 VPSRPTSSAVSTYSPITSSASSYSNTVPLTSSMDVPVYTGPDITLPPTSVMPVISP 420
QY 421 PASTQYIGIGHGTHYLLMPLYFFIPKRRKRVYFFADGFVAA 461
DB 421 PASTQYIGIGHGTHYLLMPLYFFIPKRRKRVYFFADGFVAA 461

RESULT 3

US-09-520-822A-4
Sequence 4, Application US/09520822A
Patent No. 6551597
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen
APPLICANT: Chen, Xiaojiang
TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
FILE REFERENCE: Harvard/Harrison 12687/1120
CURRENT APPLICATION NUMBER: US/09/520,822A
CURRENT FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/125208
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/148544
PRIOR FILING DATE: 1999-08-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 462

TYPE: PR1
ORGANISM: Human papillomavirus type 18
US-09-520-822A-4

Query Match 96.4%; Score 2317 5; DB 4; Length 462;
Best Local Similarity 96.8%; Pred. No. 1.6e-186;
Matches 447; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 MYSHRAARRKASVVDLYKTKQSGTCPSDVYNNKVEGTTLADKILQMSLIGIFLGIG 60
DB 1 MYSHRAARRKASVVDLYKTKQSGTCPSDVYNNKVEGTTLADKILQMSLIGIFLGIG 60
QY 61 TSSGSGRTGYIPLGSRNTVVDGTPRPVIEVGPDPISIVLIEDSSVVTSGAPP 120
DB 61 TSSGSGRTGYIPLGSRNTVVDGTPRPVIEVGPDPISIVLIEDSSVVTSGAPP 120
QY 121 TPTGSGPDTSAGTTTPAVLDITPSTSVSISTNFTNPAISDPSIIEVPTGEGAGNV 180
DB 121 TPTGSGPDTSAGTTTPAVLDITPSTSVSISTNFTNPAISDPSIIEVPTGEGAGNV 180
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DB 181 FVGTPSTGTHGEIEIPLQTFASSGTCGEPISSSTPLPTVRRVAGPRLYSRAYOVSANPE 240
QY 241 FLTRPSSLITYNPAPEVDTLTLEPRSNVDPDSDFMDIIRLRPALTSRGTVRSRIG 300
DB 241 FLTRPSSLITYNPAPEVDTLTLEPRSNVDPDSDFMDIIRLRPALTSRGTVRSRIG 300
QY 301 ORATMPTSRGQIGARVHFYHDIPTAPSEYIEIQLVSATEDNGLFTIYADDIDPAMP 360
DB 301 ORATMPTSRGQIGARVHFYHDIPTAPSEYIEIQLVSATEDNGLFTIYADDIDPAMP 360
QY 361 VPSRPTSSAVSTPSTISSASSYNNVPLTSSMDVPYTGPDITLP-PTSAWPIVSPT 419
DB 361 VPSRPTSSAVSTPSTISSASSYNNVPLTSSMDVPYTGPDITLP-PTSAWPIVSPT 419
QY 420 APASTOYIGIHGTHYLMPLFYIPKRRKRVYFFADGVAA 461
DB 420 APASTOYIGIHGTHYLMPLFYIPKRRKRVYFFADGVAA 461

RESULT 4

US-08-606-288-7
Sequence 7, Application US/08606288
Patent No. 5955087
GENERAL INFORMATION:
APPLICANT: Whittle, N.R.
APPLICANT: Carmichael, J.P.
APPLICANT: Connor, S.E.
APPLICANT: Thompson, H.S.G.
APPLICANT: Wilson, M.J.
TITLE OF INVENTION: Polypeptides Useful as Immunotherapeutic
TITLE OF INVENTION: Agents, and Methods of Polypeptide Preparation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Suite 3400, Four Embarcadero Center
CITY: San Francisco
STATE: California
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 23-FEB-1996
APPLICATION NUMBER: US/08/606,288
PRIORITY APPLICATION DATA:
FILING DATE: 24-FEB-1995
APPLICATION NUMBER: GB 9503786.7
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000034

FILING DATE: 08-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9515478.7
FILING DATE: 28-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Walter H. Dreger
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63284/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 601 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-288-7

Query Match 47.2%; Score 1134; DB 2; Length 601;
Best Local Similarity 50.8%; Pred. No. 6.2e-87;
Matches 236; Conservative 75; Mismatches 136; Indels 18; Gaps 10;

QY 5 RAARRRASVVDLYKTKQSGTCPSDVYNNKVEGTTLADKILQMSLIGIFLGIGTSG 64
DB 5 RAARRRASVVDLYKTKQSGTCPSDVYNNKVEGTTLADKILQMSLIGIFLGIGTSG 64
QY 65 TGRGTGYIPLGSRNTVVDGTP-TRPPVIEVGPDPISIVLIEDSSVVTSGAPPPTT 123
DB 65 TGRGTGYIPLGSRNTVVDGTP-TRPPVIEVGPDPISIVLIEDSSVVTSGAPPPTT 123
QY 95 TGRGTGYIPLGSRNTVVDGTP-TRPPVIEVGPDPISIVLIEDSSVVTSGAPPPTT 154
DB 95 TGRGTGYIPLGSRNTVVDGTP-TRPPVIEVGPDPISIVLIEDSSVVTSGAPPPTT 154
QY 124 GTSGPDTSAGTTTPAVLDITPSTSVSISTNFTNPAISDPSIIEVPTGEGAGNV 183
DB 124 GTSGPDTSAGTTTPAVLDITPSTSVSISTNFTNPAISDPSIIEVPTGEGAGNV 183
QY 155 AHGFTITSETTTPTAILDVSTSH-PTSTFRNPVTEBSVTOPOPEVANGHILIS 211
DB 155 AHGFTITSETTTPTAILDVSTSH-PTSTFRNPVTEBSVTOPOPEVANGHILIS 211
QY 184 TPTSGTHGEIEIPLQTFASSGTCGEPISSSTPLPTVRRVAGPRLYSRAYOVSANPE 240
DB 184 TPTSGTHGEIEIPLQTFASSGTCGEPISSSTPLPTVRRVAGPRLYSRAYOVSANPE 240
QY 212 APTTSHPTIEIPLDFVLISSSDGPTSTPVGTA-PRVGLYSRAHVOVYTDPA 268
DB 212 APTTSHPTIEIPLDFVLISSSDGPTSTPVGTA-PRVGLYSRAHVOVYTDPA 268
QY 241 FLTRPSSLITYNPAPEVDTLTLEPRSNVDPDSDFMDIIRLRPALTSRGTVRSRIG 298
DB 241 FLTRPSSLITYNPAPEVDTLTLEPRSNVDPDSDFMDIIRLRPALTSRGTVRSRIG 298
QY 269 FLSTPQRLITTYNDPYEGEDVQFSDSHIHNADEAFMDIIRLRPALTSRGTVRSRIG 328
DB 269 FLSTPQRLITTYNDPYEGEDVQFSDSHIHNADEAFMDIIRLRPALTSRGTVRSRIG 328
QY 299 LSGRATMPTSRGQIGARVHFYHDIPTAPSEYIEIQLVSATEDNGLFTIYADDIDPA 358
DB 299 LSGRATMPTSRGQIGARVHFYHDIPTAPSEYIEIQLVSATEDNGLFTIYADDIDPA 358
QY 329 IGORSMHTRSGKHICARHIFYDISPIQAAEIEMHVLVAAGEPT-FDIYANSFEPD 386
DB 329 IGORSMHTRSGKHICARHIFYDISPIQAAEIEMHVLVAAGEPT-FDIYANSFEPD 386
QY 359 MEVPSRPTSSAVSTPSTISSASS-YSNVTVPLTSSMDVPYTGPDITLPPTSWPIVS 417
DB 359 MEVPSRPTSSAVSTPSTISSASS-YSNVTVPLTSSMDVPYTGPDITLPPTSWPIVS 417
QY 387 INPTQHPVTNINISDTYLTSTPNVTQPMGNTVPLSIPNDLFLQSGPDITFPTAPMGTPS 446
DB 387 INPTQHPVTNINISDTYLTSTPNVTQPMGNTVPLSIPNDLFLQSGPDITFPTAPMGTPS 446
QY 418 PTAPA-STOYIGIHGTHYLMPLFYIPKRRKRVYFFADGVAA 461
DB 418 PTAPA-STOYIGIHGTHYLMPLFYIPKRRKRVYFFADGVAA 461
QY 447 PVTPLPTGVPFTSGFYLHPAWFYARRRRRIPLFSD-VAA 489
DB 447 PVTPLPTGVPFTSGFYLHPAWFYARRRRRIPLFSD-VAA 489

RESULT 5

US-08-606-288-10
Sequence 10, Application US/08606288
Patent No. 5955087
GENERAL INFORMATION:
APPLICANT: Whittle, N.R.
APPLICANT: Carmichael, J.P.
APPLICANT: Connor, S.E.
APPLICANT: Thompson, H.S.G.
APPLICANT: Wilson, M.J.
TITLE OF INVENTION: Polypeptides Useful as Immunotherapeutic
TITLE OF INVENTION: Agents, and Methods of Polypeptide Preparation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Suite 3400, Four Embarcadero Center
CITY: San Francisco


```

Db      2659 FLSTQORLITVYDNPNFYEGEDVDVSQSHSIHNAPEAFNDIIRLRHPALASRGRLRYSR   328
Oy      299 IGRARNTMTRSGTQIGARVHFHDISPIAPSEFYELEQPLVSATEDNGELDIYADDIDPA   358
        :|::||| |||:::|||::| |::|||::| |::|||::| |::|||::|
Db      329 IGORSMTTRSCKHGRIARIHYEYDISPIQAEEIEEMHPLVAQAQEDT--FDIAKSFEPD   386
Oy      359 MPVSRPTTSSAVSVSYSPTISSASS-YSNWVYPLTSSMDVPYYTGPDILPPTSVMPIYS   417
        :|::|||::| |::|||::| |::|||::| |::|||::| |::|||::|
Db      387 INPTGHPATNIDSITYLTSPNTVTTPDPWGATTYPLEIPNDLFQSOGSDITFFPAPMGTPRS   446
Oy      418 PLAPA-STQYIGIHGTHTLYMLPYEIFPKRRRVYFPADGVAA   461
        | |::|||::| |::|||::| |::|||::| |::|||::|
Db      447 PVTPLPTGPVYTTTOSCFYLHAMIFARRRKRRIPLFESD--VAA   489

RESULT 7
US-09-347-483-10
? Sequence 10, Application US/09347483
? Patent No. 6123948
GENERAL INFORMATION:
APPLICANT: Whittle, N.R.
APPLICANT: Carmichael, J.P.
APPLICANT: Connor, S.E.
APPLICANT: Thompson, H.S.G.
APPLICANT: Wilson, M.J.
TITLE OF INVENTION: Polypeptides Useful as Immunotherapeutic
TITLE OF INVENTION: Agents, and Methods of Polypeptide Preparation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Flehr, Hobbach, Test, Albritten & Herbert
STREET: Suite 3400, Four Embaradero Center
CITY: San Francisco
STATE: California
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/347,483
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/606,288
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000034
FILING DATE: 08-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9515478.7
FILING DATE: 28-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Walter H. Dreger
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63284/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 601 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-347-483-10

Query Match          47.2%; Score 1134; DB 3; Length 601;
Best Local Similarity 50.8%; Pred. NO. 6,2e-87;
Matches 236; Conservative 75; Mismatches 136; Indels 18; Gaps 10;

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[illegible]

```

RESULT 8
US-09-520-822A-2
: Sequence 2, Application US/09520822A
: Patent No. 6551597
: GENERAL INFORMATION:
: APPLICANT: Harrison, Stephen
: APPLICANT: Chen, Xiaojiang
: TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
: TITLE OF INVENTION: virus
: FILE REFERENCE: Harvard/Harrison 12687/1120
: CURRENT APPLICATION NUMBER: US/09/520,822A
: CURRENT FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/125208
: PRIOR FILING DATE: 1999-03-18
: PRIOR APPLICATION NUMBER: 60/148544
: PRIOR FILING DATE: 1999-08-12
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 473
: TYPE: PRN
: ORGANISM: Human papillomavirus type 16
: US-09-520-822A-2

```

	Query Match	47.1%;	Score 1133.5;	DB 4;	Length 473;
	Best Local Similarity	49.2%;	Pred. No. 4.8e-87;		
	Matches	237;	Conservative 73;	Mismatches 131;	Indels 41; Gaps 12;
QY	6	AARRRASVTDLYKTCROSGCTPSDVKVAVKGTLLADILDMSSLGIFLAGIGTIGTSGCT	65		
	7	AKRRKRASADOLYKTCROAGCTCPDILPKVEGKTIAREQILLYGSMGVEFGGIGTIGTSGCT	66		
QY	66	GGRTGYIPLIGRSMTVVD-VGPTRPVYIEVGPTDSIVYLIEDSSVYTGAR--PTF	122		
	67	GGRTGYIPLIGRPPATDITLAPVPRPPLVDVGPSPDSIVLVEETSEIDGALPYSVRSI	126		
QY	123	-TGTSGFDITSAGTTTPAVLIDFTSSVSISITNTFNPAPASDSIIEVPOTGSGAVWF	181		
QY	127	PPDVSGRSITTSSTDTTPALIDNNVTTV-----TTHNNPTITDSVLPAPPAETGGHFT	182		
QY	182	VGPTSGTGTGEEELPLDTFASSGCGEEPISSTPLPYARRVAGPRLYSRAVQOVSVAANEF	241		


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Db      6 RYKRASAYDLKRTCKOAGCPDPVIRKVEGDTIAKILKFGALATYLGSLGIGTWSGTV 65
QY      64 GTGRTGYIPL--GGRSNTVVDVGP-----TRPV-----VIEPVPTPST---VT 105
Db      66 AAGGSPRYPLRTAGTSSLASISGRNAVYAGTRPSIGAGIPDITLTTALALRPGVEDTV 125
QY      106 LIESSVVTSGAPRPTFTGSGFDITSAGTTP-----AVLDTP-SST 148
Db      126 LPEAPAIYTPDA-----VPADSGDALISTDSSTELLITLLEPEGEDIAVLELOPLDRP 181
QY      149 SVSISTNTNPAFSDPSIIEVPQGEVSG--NVFVGTPTSGTHGEELIPLQTFASSGTV 206
Db      182 TWQVSNAAVQSSAYHAPLOLO--SIAETSGLENIIEVGGSGLDGTGGENIELTAYFGS---- 236
QY      207 EEPISSTPLPYTRRVAGPRLY--SRAYQOVYANPEFLRPSLITYDPAPEPVDTTLT 264
Db      237 --PRISTPRSIASKSGILNMFSSKRYTYQVPEDEPV-----SSQTFANPLEA----- 284
QY      265 FEPRSNVPDSDPMDIIRLHRPALTSRGTVRFSRLGQRATMFTSGTOIGANVHFYHDIS 324
Db      285 -EP-----AVLKGPSGVRGLSQYKKPDLTTRSGTEVGPQLHVRYSLS 326
QY      325 PIAPSPRYT-----ELQPLVSATEDNGLEFDIYADDDPA--MP----- 360
Db      327 TTHEDVEALPYVDENTOGIAFVPL--HEEQAGFEIEILDSETHRLLPQNTSSTPVGS 384
QY      361 -----VPSR---PTTSSAVSYT-SPTISSASSYSNVYPLNLSMDVPYTYGPDITLPT 410
Db      385 GVRSLIPIRERSATRPCTGVVYTGSPDYTSAS-----PVND---POSTSPSLVIDDT 433
QY      411 SWMPIVSPAPASTOYIGIGHYHYLMPLYYFIPKRRK 448
Db      434 TTTPII-----IDGHTVDLYSSNYTLHPSLLRKRRK 467

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RESULT 11
US-09-479-645A-8
; Sequence 8, Application US/09479645A
; Patent No. 6489141
; GENERAL INFORMATION:
; APPLICANT: PRAZER, Ian Hector
; APPLICANT: ZHOU, Jian
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AND METHOD FOR SELECTIVELY
; FILE REFERENCE: 210338.0001/US
; CURRENT APPLICATION NUMBER: US/09/479,645A
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: PCT/AU98/00530
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: AU P07765
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: AU P09467
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bovine
; OTHER INFORMATION: papillomavirus type 1 L2 open reading frame
; OTHER INFORMATION: (humanized)
; OTHER INFORMATION: Wild-type codons replaced with synonymous codons
; OTHER INFORMATION: used at relatively high frequency by human genes
US-09-479-645A-8

```

Query Match 17.0%; Score 408.5; DB 4; Length 469;
 Best Local Similarity 29.3%; Pred. No. 3.8e-26;
 Matches 152; Conservative 59; Mismatches 174; Indels 133; Gaps 24;

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QY      8 RYKRASAYDLKRTCKOAGCPDPVIRKVEGDTIAKILKFGALATYLGSLGIGTWSGTV 63
Db      6 RYKRASAYDLKRTCKOAGCPDPVIRKVEGDTIAKILKFGALATYLGSLGIGTWSGTV 65
QY      64 GTGRTGYIPL--GGRSNTVVDVGP-----TRPV-----VIEPVPTPST---VT 105
Db      66 AAGGSPRYPLRTAGTSSLASISGRNAVYAGTRPSIGAGIPDITLTTALALRPGVEDTV 125
QY      106 LIESSVVTSGAPRPTFTGSGFDITSAGTTP-----AVLDTP-SST 148
Db      126 LPEAPAIYTPDA-----VPADSGDALISTDSSTELLITLLEPEGEDIAVLELOPLDRP 181
QY      149 SVSISTNTNPAFSDPSIIEVPQGEVSG--NVFVGTPTSGTHGEELIPLQTFASSGTV 206
Db      182 TWQVSNAAVQSSAYHAPLOLO--SIAETSGLENIIEVGGSGLDGTGGENIELTAYFGS---- 236
QY      207 EEPISSTPLPYTRRVAGPRLY--SRAYQOVYANPEFLRPSLITYDPAPEPVDTTLT 264
Db      237 --PRISTPRSIASKSGILNMFSSKRYTYQVPEDEPV-----SSQTFANPLEA----- 284
QY      265 FEPRSNVPDSDPMDIIRLHRPALTSRGTVRFSRLGQRATMFTSGTOIGANVHFYHDIS 324
Db      285 -EP-----AVLKGPSGVRGLSQYKKPDLTTRSGTEVGPQLHVRYSLS 326
QY      325 PIAPSPRYT-----ELQPLVSATEDNGLEFDIYADDDPA--MP----- 360
Db      327 TTHEDVEALPYVDENTOGIAFVPL--HEEQAGFEIEILDSETHRLLPQNTSSTPVGS 384
QY      361 -----VPSR---PTTSSAVSYT-SPTISSASSYSNVYPLNLSMDVPYTYGPDITLPT 410
Db      385 GVRSLIPIRERSATRPCTGVVYTGSPDYTSAS-----PVND---POSTSPSLVIDDT 433
QY      411 SWMPIVSPAPASTOYIGIGHYHYLMPLYYFIPKRRK 448
Db      434 TTTPII-----IDGHTVDLYSSNYTLHPSLLRKRRK 467

```

```

RESULT 12
US-08-484-791-2
; Sequence 2, Application US/08484791
; Patent No. 6380157
; GENERAL INFORMATION:
; APPLICANT: Jarrett, William F.H.
; APPLICANT: Campo, Maria S.
; APPLICANT: Smith, Kenneth T.
; TITLE OF INVENTION: Papillomavirus L2 protein
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Flehr Hobach Test Albritton & Herbert LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,791
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/170,185
; FILING DATE: 29-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01092
; FILING DATE: 17-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9113809.9
; FILING DATE: 26-JUN-1991
; ATTORNEY/AGENT INFORMATION:

```

NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-59687-1/MHD/MTK
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3329
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 964 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-484-791-2

Query Match 15.8%; Score 380.5; DB 4; Length 964;
 Best Local Similarity 28.3%; Pred. No. 2,4e-23;

Matches 149; Conservative 56; Mismatches 187; Indels 135; Gaps 24;

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QY 8 RRRRASTDLKTKCKSGCTCPDVYKVEGTTLADKILQWSSLGIFLGIGTGS--- 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 RVRANAYDLYRTCKQKGTCPDPVIFPEEDTADKILKGLAIGLAIIGTWTGTV 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 64 GTGRTGYIDL--GGRSTVVDVGP-----TR-----PVVIEEVGPTDEI---VT 105
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 AAGGSPRYVPLKRTSGSTSLASVGRAGAARTRSSITGIPDLDTLETIGALRPAVEDTV 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 106 LIESSVSVISGAPRPETGTSGFDI--TSAGITT-----PAVLDTTP--SSTSVS 151
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 126 LPEAPALVETDAV--PADTGIDGLSIGDSTETLITLLEPEGPDAVLEQLPDHANMQ 184
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 152 ISTTNFNPAPSDPSITIEVQGTGVSQ--NVEVGTPIPSGTHGYEHLPLQTPASSGTGEEP 209
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 185 VSNANVQGSAYHAPLQIQ--SSIAETSGLENIPEVGAGLGDGTGENIELITFEFGS-----P 237
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 210 ISSPT--LPTVRRVAGRLTSRAYQVSVANPEFLTPSSLITTDNPAFEPVDTTLTEEP 267
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 238 RTSTPRALPQTANGILNMFESKRYTQIPTEDPVF-----SSQTSNAYVD-----EP 286
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 268 RSNVPDSDPMDIIRLHRPALTSRGTVRSRLQQRATMTFRSGTQIGARVHFYHDISPIA 327
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 287 -----AVLKGPSRGVGLQVYVRPDYETRRGGQVGPQLHVRSLSTIT 329
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 328 PSPEYIELQPLVATENGFL-----DIYADDI-----DPAMPVPS--- 363
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 330 ---EDVEALPIAVDEDTQGLAFLPLHEEPDFEEIELDDIGEHALPKSSTAPIGSGVR 386
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 364 -----RPTSSAVSTY--SPTISSASSYSNTVPLTSSMDVPYTTGPDITLPT 410
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 387 RALIPGGGFSATRPT---GYVTYGSPPDMYPASPVG-----PDSTSPSLVTDN 431
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 411 SWMPIVSPFAPASTQYIGIHGYIYMLPYTFIPKKRVPYFFADG 457
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 432 TTPPIII---IDGHVTDLYSNYSILHPSILRRKKRHHAMALMOQG 474
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

RESULT 13

US-09-556-706B-2
 Sequence 2, Application US/09556706B
 Patent No. 6458364
 GENERAL INFORMATION:
 APPLICANT: Spaete, Richard
 APPLICANT: Jackman, Winthrop
 TITLE OF INVENTION: NON SPLICING VARIANTS OF GP350/220
 FILE REFERENCE: 7682-050-999
 CURRENT APPLICATION NUMBER: US/09/556,706B
 CURRENT FILING DATE: 2000-04-24
 PRIOR APPLICATION NUMBER: 08/783,774
 PRIOR FILING DATE: 1997-01-15
 PRIOR APPLICATION NUMBER: 08/229,291
 PRIOR FILING DATE: 1994-04-18
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2

LENGTH: 878
 TYPE: PRT
 ORGANISM: Virus
 FEATURE:
 OTHER INFORMATION: GP350
 US-09-556-706B-2

Query Match 6.3%; Score 151; DB 4; Length 878;
 Best Local Similarity 22.9%; Pred. No. 0.0004;
 Matches 115; Conservative 52; Mismatches 164; Indels 172; Gaps 25;

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QY 18 YKTCCKSG---TCPSDVYKVEGTTLADKI--LQWSSLGIFLGIGI-----GTGSGTGC 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 235 YESHVPSGGILTSRSPATPIPGYAVSLRTPRPVSRRLGNNSILYVYSGNGPRAAG 294
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 68 RTGIPLPGISNNYV--VVGTPRPVYLEPGDPDSIVTLEDS-----VYTS---GAP 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 295 GDYCI---OSNIVSEIIPASQDM-----PINTDTIYVGDNATYSVPMYVSEDANSP 344
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 119 RPPTG-----TSG-----FDITSAGT--TTPAVLD 142
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 345 NVTYTAFWAMPNNTEPDFCKKWTLSGTPSGCENISAFASNRFTDITVSGLGTAPEKTLI 404
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 143 ITBSSTSVSIST-----TNFTNP-----AFSDPSITE--VPQTEVSGNVEVGTPT 186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 405 ITRATNATTTTHKVIKAPDESTTSPITNTGTFAFPNTTGLPSSTHVPTNLAPAST 464
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 187 SGTGYEHLPLQTPASSGTGEEPISRPPLTVRRVAGPRLXRAYQVSVANPEFLTRPS 246
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 465 GPVSTADVTSPTPAGTSGASPVTPSPSPMDNGTE-----SKAPDMTSSSTP--VTTPT 517
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 247 SLITYDNPAFEPVDTTLTFEPRSNVPSDPMIDIIRLHRPALTSRGTVRSRLQQRATMF 306
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 518 PNATSPTRAV---TTPPT--PNATSP-----TPAVTPTPNATSPTLGK----- 555
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 307 TRSGTQIGARVHFYHDISPIAPSPYELEOLPLVSATDNGFLFDIYADDIDPAMPVPSRPT 366
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 556 -----TSPTSAVTTPTPNATSP-----PTLGKTS 578
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 367 TSSAVST-----XSPTISSASSYSNTVPLTSSMDVPYVYGPDI-----TLP 409
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 579 PTAIVTTPTPNATSPTLGKTSPTSAVTTP-----TPNATGPVGETSPQANATNHTLGG 632
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 410 TSWMPIVS--PTAPASTQYIGIH 430
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 633 TSPPTVVTISQPKNATSAVTTGQH 655
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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RESULT 14

US-08-783-774-2
 Sequence 2, Application US/08783774
 Patent No. 6054130
 GENERAL INFORMATION:
 APPLICANT: Spaete, Richard
 APPLICANT: Jackman, Winthrop
 TITLE OF INVENTION: NON-SPLICING VARIANTS OF
 NUMBER OF INVENTION: GP350/220
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036/2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/783,774
 FILING DATE: 15-JAN-1997

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-037
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 907 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-783-774-2

Query Match 6.3%; Score 151; DB 3; Length 907;
Best Local Similarity 22.9%; Pred. No. 0.00042;
Matches 115; Conservative 52; Mismatches 164; Indels 172; Gaps 25;

18 YKTCRQSG--TCSPDVNKEGTTLADKI-LQWSSLGIFLGIGI-----GTSGGTG 67
235 YESHVSQGLITSTSPVATPIPGTGYASRLPRPVSRGLNNSILYVYSGNGPKASG 294
68 RTGIYPLGGRSNTV-DVGPTRPVYIEPVGPTDPSIVTLIEDSS---VWTS---GAP 118
295 GDYCI-----OSNIVFSDIPIASQDM-----PTNTDITYVGNATVSPMTSEDA NSP 344
119 RPTFTG-----TSG-----EDITSAGT--TPRAVID 142
345 NVTVIAFWAMPNNTETDFCKKWLITSGTPSGCENISGAFASNRTFDITVSGLTAPKTLI 404
143 ITSPSTSVSIST-----TNTNP-----AFSDPSITE--VPOTGEVSGNVFVCTPT 186
405 ITRATNATTTTHKVIIFSKAPESTTSPILNTGTFADPNTTGLPSTHVPNTLNITAPAST 464
187 SGTHGEIEIPLOTFPSSGTEGEEPISTPLPTVRRVAGPRLYSRAYQOVSVANPEFLTRPS 246
465 GPTVSTADVTSPTPAGTTSASPVTPSPSPWMDNGTE-----SKAPDMTSTSP--VTTPT 517
247 SLITYDNPAPEPVDITLTFPRSNVPSDPMOILRLHRPALTSRGRVRSRIGQRATMF 306
518 PNATSPTRAV-----TPATTPTPNATSP-----TPAVTTPTPNATSP-----PTLAKTS 578
307 TRSGTQIGARVHFYHDISPIAPSPREYIELOPLVSATEDNGLFDIYADDIDPAMPVPSRPT 366
556 -----TSPTSAVTTPTPNATSP-----PTLAKTS 578
367 TSSAVST-----YSPITSSASYSNVTVPILTSMVDVPTYGPD-----TLPP 409
579 PTAIVTTPTPNATSPILGKTSPTSAVTTTP-----TPNATGPTVGETSPQANATNHTLGG 632
410 TSWPPIVS--PTAPASQYIGIH 430
633 TSPTPVVTSPQKNATSAVTTGQH 655

RESULT 15
US-09-328-599A-1
Sequence 1, Application US/09328599A
Patent No. 6432679
GENERAL INFORMATION:
APPLICANT: MOND, James J. and Tees, Andrew
TITLE OF INVENTION: Enhancement of B Cell Activation by
TITLE OF INVENTION: Co-ligation of Receptors for Antigen and Complement C3d
TITLE OF INVENTION: Using EBV gp350/220 or EBV gp350/220 Peptide Adjuncts
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunnet, L.L.P.
STREET: 1300 I Street, N.W., Suite 700

CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,599A
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 04995.6025-00000
TELEPHONE: (202)408-4000
TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 907 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-328-599A-1

Query Match 6.3%; Score 151; DB 4; Length 907;
Best Local Similarity 22.9%; Pred. No. 0.00042;
Matches 115; Conservative 52; Mismatches 164; Indels 172; Gaps 25;

18 YKTCRQSG--TCSPDVNKEGTTLADKI-LQWSSLGIFLGIGI-----GTSGGTG 67
235 YESHVSQGLITSTSPVATPIPGTGYASRLPRPVSRGLNNSILYVYSGNGPKASG 294
68 RTGIYPLGGRSNTV-DVGPTRPVYIEPVGPTDPSIVTLIEDSS---VWTS---GAP 118
295 GDYCI-----OSNIVFSDIPIASQDM-----PTNTDITYVGNATVSPMTSEDA NSP 344
119 RPTFTG-----TSG-----EDITSAGT--TPRAVID 142
345 NVTVIAFWAMPNNTETDFCKKWLITSGTPSGCENISGAFASNRTFDITVSGLTAPKTLI 404
143 ITSPSTSVSIST-----TNTNP-----AFSDPSITE--VPOTGEVSGNVFVCTPT 186
405 ITRATNATTTTHKVIIFSKAPESTTSPILNTGTFADPNTTGLPSTHVPNTLNITAPAST 464
187 SGTHGEIEIPLOTFPSSGTEGEEPISTPLPTVRRVAGPRLYSRAYQOVSVANPEFLTRPS 246
465 GPTVSTADVTSPTPAGTTSASPVTPSPSPWMDNGTE-----SKAPDMTSTSP--VTTPT 517
247 SLITYDNPAPEPVDITLTFPRSNVPSDPMOILRLHRPALTSRGRVRSRIGQRATMF 306
518 PNATSPTRAV-----TPATTPTPNATSP-----TPAVTTPTPNATSP-----PTLAKTS 578
307 TRSGTQIGARVHFYHDISPIAPSPREYIELOPLVSATEDNGLFDIYADDIDPAMPVPSRPT 366
556 -----TSPTSAVTTPTPNATSP-----PTLAKTS 578
367 TSSAVST-----YSPITSSASYSNVTVPILTSMVDVPTYGPD-----TLPP 409
579 PTAIVTTPTPNATSPILGKTSPTSAVTTTP-----TPNATGPTVGETSPQANATNHTLGG 632
410 TSWPPIVS--PTAPASQYIGIH 430
633 TSPTPVVTSPQKNATSAVTTGQH 655

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